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OM nucleic - nucleic search, using sw model

Run on: February 22, 2005, 19:20:42 ; Search time 110 Seconds
(without alignments)
8895.395 Million cell updates/sec

Title: US-09-920-953-2
Perfect score: 598
Sequence: 1 ggctcctgcagacggc.....agccatttcgaccaagcc 598

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97.2	16.3	381	4	US-09-902-540-5776 Sequence 5776, Ap
2	97.2	16.3	72704	4	US-09-902-540-1273 Sequence 1273, Ap
3	46.4	7.8	4403765	3	US-09-103-840A-2 Sequence 2, Appli
4	46.4	7.8	4411529	3	US-09-103-840A-1 Sequence 1, Appli
5	45.2	7.6	1143	4	US-09-902-540-8600 Sequence 8600, Ap
6	45.2	7.6	6821	4	US-09-902-540-907 Sequence 907, App
7	43.4	7.3	603	4	US-09-902-540-14 Sequence 14, Appl
8	43.4	7.3	603	4	US-09-902-540-5853 Sequence 5853, Ap
9	42.8	7.2	585	4	US-09-902-540-3555 Sequence 3555, Ap
10	42.8	7.2	19019	4	US-09-902-540-1171 Sequence 1171, Ap
11	42.6	7.1	3128	4	US-09-744-072-1 Sequence 1, Appli
12	42.4	7.1	26896	4	US-09-949-016-16800 Sequence 16800, A
13	42.2	7.1	759	4	US-09-252-991A-11092 Sequence 11092, A
14	42	7.0	1058	3	US-09-452-239-11 Sequence 11, Appl
15	41.6	7.0	969	4	US-09-902-540-8164 Sequence 8164, Ap
16	41.6	7.0	1280	3	US-09-096-776B-4 Sequence 4, Appli
17	41.6	7.0	1280	4	US-09-923-922-4 Sequence 4, Appli
18	41.6	7.0	1491	3	US-09-082-092-9 Sequence 9, Appli
19	41.6	7.0	1491	4	US-09-885-722A-9 Sequence 9, Appli
20	41.6	7.0	1524	3	US-08-840-767-3 Sequence 3, Appli
21	41.6	7.0	1817	3	US-09-288-292A-45 Sequence 45, Appl
22	41.6	7.0	2887	4	US-09-679-298A-1 Sequence 1, Appli
23	41.6	7.0	3083	2	US-08-480-994-36 Sequence 36, Appl
24	41.6	7.0	3083	2	US-08-616-844-36 Sequence 36, Appl
25	41.6	7.0	3083	2	US-08-599-654-36 Sequence 36, Appl
26	41.6	7.0	3083	2	US-08-485-573-36 Sequence 36, Appl
27	41.6	7.0	3083	3	US-08-944-868A-36 Sequence 36, Appl

28	41.6	7.0	3083	3	US-08-944-423A-36 Sequence 36, Appl
29	41.6	7.0	3083	3	US-08-925-743-36 Sequence 36, Appl
30	41.6	7.0	3083	3	US-08-944-496-36 Sequence 36, Appl
31	41.6	7.0	3083	3	US-08-925-767-36 Sequence 36, Appl
32	41.6	7.0	3084	3	US-08-826-246-11 Sequence 11, Appl
33	41.6	7.0	3084	3	US-08-944-495-11 Sequence 11, Appl
34	41.6	7.0	3084	3	US-09-126-640-6 Sequence 6, Appli
35	41.6	7.0	3084	3	US-08-925-588-11 Sequence 11, Appl
36	41.6	7.0	3084	3	US-09-288-292A-6 Sequence 6, Appli
37	41.6	7.0	3084	4	US-09-372-044-11 Sequence 11, Appl
38	41.6	7.0	3084	4	US-08-825-486-11 Sequence 11, Appl
39	41.6	7.0	3084	4	US-08-826-248-11 Sequence 839, App
40	41.6	7.0	5663	4	US-09-902-540-839 Sequence 9635, Ap
41	41.2	6.9	3066	4	US-09-902-540-9635 Sequence 1094, Ap
42	41.2	6.9	15782	4	US-09-902-540-1094 Sequence 9640, Ap
43	41	6.9	1440	4	US-09-902-540-1094 Sequence 1094, Ap
44	41	6.9	15782	4	US-09-902-540-1094 Sequence 10543, A
45	40.8	6.8	792	4	US-09-252-991A-10543

ALIGNMENTS

RESULT 1
US-09-902-540-5776
; Sequence 5776, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5776
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5776

Query Match	16.3%;	Score	97.2;	DB	4;	Length	381;
Best Local Similarity	56.9%;	Pred. No.	2.7e-17;				
Matches	199;	Conservative	0;	Mismatches	148;	Indels	3;
Gaps							
QY	61	AAGAAGCTGTTT	GATGACCTTGGCGGCGCAGAGGATGAAGCTGGCGGTGACACCTTC	120			
DB	19	AAGAGTGTCT	TACAGCAGCTGGCGGAGAGCCGCGGTGGAGGTCTTC	78			
QY	121	TACGATAAGGTGCTGCTGACCCGAGAGTCTGCTCCCTTTTCGAGTCCCTGGACATGCAA	180				
DB	79	TACCGGAAGTGTGCTGCGGAGCATCATCAGCCACTTCTTCGAGGACGTGGACATGGAG	138				
QY	181	GACGAGAGTGAAGCAGGTCAAGTTTCATGAGTTCGTTTGGCGGAGCAGACCAATAC	240				
DB	139	CGCCAGCGCCGGAAGCAGAGGCGTTCCTGACATGTTGACGGGTGGCGCGGTCCATC	198				
QY	241	AAGGGCGGAAGCATGTACGACGACACCGCCATCTGCTCAAGGGCCACGCGCTGGACCA	300				
DB	199	TCGGGAGAGCATGCGCGGCGCCACGCGCTCTGTTGAG---	255				
QY	301	CGCCACTTTGACAAAGATCAAGCAGTACCTTTGGAGACGCTGCAAGAGATGGCGCTCAAG	360				
DB	256	TCGCACTTCGACGCGGTGGCGGCCACCTGAAGCGACGCTGGAGGAGCTGGCGCTGCC	315				
QY	361	CAGGATGTGATCCAGACGCGCGGAGTGTGAGTCCACCCGCGGACGA	410				
DB	316	GCGCCGCTGTTGGCGAGGTGATGACCATCGCGGAGAGCGCCCGCGGGA	365				

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; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      7.8%; Score 46.4; DB 3; Length 4403765;
Best Local Similarity 50.9%; Pred. No. 0.11; Mismatches 106; Indels 0; Gaps 0;
Matches 110; Conservative 0;

QY 51 ATCGGGCGCAAGAAGCTGTTTGATGACCTGGGCGCGCAGAGCATGAAGCTGGCGGT 110
DB 1744933 ACGTGAGCCGATCAGCATCTACGACAAGATCGGGCGGCGATCGAAGTCGTCGT 1744874

QY 111 TGACACCTTCTACGATAAGGTGCTGCTGAGCCGAGAGCTGCTGCCCTTCTTCGAGTCCCT 170
DB 1744873 CGAGGACTTCTATGTTGCTGCTTGGCGATGACCAACTATCGGCCTTCTTCAGCGGTAC 1744814

QY 171 GGACATGCAGAGCAGAGATGAGCAGGTCAAGTTCATGAGCTTCGTTGTCGGGAGC 230
DB 1744813 GAACATGAGCGCCTCAAGGGCAAGCAGGTGGAGTGTTCGCGCCGCGCTTGGCGGCC 1744754

QY 231 AGACCAATACAAAGGCGCGAAGCATGTACGAGCGACA 266
DB 1744753 CGAGCCCTATACCGTGGCGCGATGAAGCAAGTCCA 1744718

RESULT 4
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      7.8%; Score 46.4; DB 3; Length 4411529;
Best Local Similarity 50.9%; Pred. No. 0.11; Mismatches 106; Indels 0; Gaps 0;
Matches 110; Conservative 0;

QY 51 ATCGGGCGCAAGAAGCTGTTTGATGACCTGGGCGCGCAGAGCATGAAGCTGGCGGT 110
DB 1744808 ACGTGAGCCGATCAGCATCTACGACAAGATCGGGCGGCGATCGAAGTCGTCGT 1744749

QY 111 TGACACCTTCTACGATAAGGTGCTGCTGAGCCGAGAGCTGCTGCCCTTCTTCGAGTCCCT 170
DB 1744748 CGAGGACTTCTATGTTGCTGCTTGGCGATGACCAACTATCGGCCTTCTTCAGCGGTAC 1744689

QY 171 GGACATGCAGAGCAGAGATGAGCAGGTCAAGTTCATGAGCTTCGTTGTCGGGAGC 230
DB 1744688 GAACATGAGCGCCTCAAGGGCAAGCAGGTGGAGTGTTCGCGCCGCGCTTGGCGGCC 1744629

QY 231 AGACCAATACAAAGGCGCGAAGCATGTACGAGCGACA 266
DB 1744628 CGAGCCCTATACCGTGGCGCGATGAAGCAAGTCCA 1744593

; SEQ ID NO 2

US-09-902-540-1273
; Sequence 1273, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902.540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1273
; LENGTH: 72704
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72704)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1273

Query Match      16.3%; Score 97.2; DB 4; Length 72704;
Best Local Similarity 56.9%; Pred. No. 2e-16; Mismatches 148; Indels 3; Gaps 1;
Matches 199; Conservative 0;

QY 61 AAGAAGCTGTTTGATGACCTGGGCGCGCAGAGCATGAAGCTGGCGGTTCACACCTTC 120
DB 21785 AAGAAGCTGTTTGATGACCTGGGCGCGCAGAGCATGAAGCTGGCGGTTCACACCTTC 21844

QY 121 TACGATAAGGTGCTGCTGACCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATGCAA 180
DB 21845 TACCGAAGGTGCTGGCGAGCATCACATCAGCCACTTCTTCGAGGACGTGGACATGAG 21904

QY 181 GAGCAGAGATGAAGAGTCAAGTTCATGACTTCGTTGTTGGGCGGAGCAGACCAATAC 240
DB 21905 CGCCAGCGCGCAAGCAGAGCGTTCCTGACGATGGTGACGGGTGGCGCGGTCCACTAC 21964

QY 241 AAGGCGGAAGCATGTACACACACAGCGCCATCTGTTCAAGGGCCACGCGCTGGACAC 300
DB 21965 TCGGCAAGGACATGCGCGCGGCGCACGCGCTCTGTTGAAG--CGTGGCTGAACGAC 22021

QY 301 CGCCACTTTGACAAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAG 360
DB 22022 TCGCACTTCAGCGGTGGCGGCGCACCTGAAGGGCGACGCTGGAGGAGCTGGGCGTGGCC 22081

QY 361 CAGGATGATCAGACACCGCGCGGAGTGGTGGAGTCCACCGCGACA 410
DB 22082 GCGCGCTGTTGGCGGAGGTGATGACCATCGCGGAGAGCGCGCGCGGA 22131

RESULT 3
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
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; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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Query Match      7.8%; Score 46.4; DB 3; Length 4403765;
Best Local Similarity 50.9%; Pred. No. 0.11; Mismatches 106; Indels 0; Gaps 0;
Matches 110; Conservative 0;

QY 51 ATCGGGCGCAAGAAGCTGTTTGATGACCTGGGCGCGCAGAGCATGAAGCTGGCGGT 110
DB 1744933 ACGTGAGCCGATCAGCATCTACGACAAGATCGGGCGGCGATCGAAGTCGTCGT 1744874

QY 111 TGACACCTTCTACGATAAGGTGCTGCTGAGCCGAGAGCTGCTGCCCTTCTTCGAGTCCCT 170
DB 1744873 CGAGGACTTCTATGTTGCTGCTTGGCGATGACCAACTATCGGCCTTCTTCAGCGGTAC 1744814

QY 171 GGACATGCAGAGCAGAGATGAGCAGGTCAAGTTCATGAGCTTCGTTGTCGGGAGC 230
DB 1744813 GAACATGAGCGCCTCAAGGGCAAGCAGGTGGAGTGTTCGCGCCGCGCTTGGCGGCC 1744754

QY 231 AGACCAATACAAAGGCGCGAAGCATGTACGAGCGACA 266
DB 1744753 CGAGCCCTATACCGTGGCGCGATGAAGCAAGTCCA 1744718
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RESULT 4
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Query Match      7.8%; Score 46.4; DB 3; Length 4411529;
Best Local Similarity 50.9%; Pred. No. 0.11; Mismatches 106; Indels 0; Gaps 0;
Matches 110; Conservative 0;

QY 51 ATCGGGCGCAAGAAGCTGTTTGATGACCTGGGCGCGCAGAGCATGAAGCTGGCGGT 110
DB 1744808 ACGTGAGCCGATCAGCATCTACGACAAGATCGGGCGGCGATCGAAGTCGTCGT 1744749

QY 111 TGACACCTTCTACGATAAGGTGCTGCTGAGCCGAGAGCTGCTGCCCTTCTTCGAGTCCCT 170
DB 1744748 CGAGGACTTCTATGTTGCTGCTTGGCGATGACCAACTATCGGCCTTCTTCAGCGGTAC 1744689

QY 171 GGACATGCAGAGCAGAGATGAGCAGGTCAAGTTCATGAGCTTCGTTGTCGGGAGC 230
DB 1744688 GAACATGAGCGCCTCAAGGGCAAGCAGGTGGAGTGTTCGCGCCGCGCTTGGCGGCC 1744629

QY 231 AGACCAATACAAAGGCGCGAAGCATGTACGAGCGACA 266
DB 1744628 CGAGCCCTATACCGTGGCGCGATGAAGCAAGTCCA 1744593

; SEQ ID NO 2
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RESULT 5
US-09-902-540-8600
; Sequence 8600, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8600
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-8600

Query Match      7.6%; Score 45.2; DB 4; Length 1143;
Best Local Similarity 45.5%; Pred. No. 0.011;
Matches 158; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 82 GCGCGCGCAGAGCATGAAGCTGGCGGTTGACACCTTCTACGATAAGGTGCTGGCTGAC 141
Db 169 GGGCTGCTCGCGCGGAGGCGCTGGCGACGTGCTGTTCCACGACAGCGGCCCTGTCAAGC 228
QY 142 CCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGAGATCAAGAGAGAGATGAAGCAGGTC 201
Db 229 TGGCGGACGGTGTCTCGCGAGTGCCTGCGGAGTGCCTGCGGAGGCGCTGACGTTGCCACCGCC 288
QY 202 AAGTTTCATGAGCTTCTGTTGGCGGAGCAGACCAATACAAAGGCGCCGAAAGCATGTAGCAC 261
Db 289 AAGGCCAAGGGCTCGGACGGACACCTGTCGAGGCGCAACCCGCCACCTGCTGAAAGCTG 348
QY 262 GCACACGCCCATCTGTTCAAGGGCCACCGCTTGAGAGATCAAGGCGCCGAAAGCATGTAGCAC 321
Db 349 GCCTACAAACCGCTGTTTCATGTGGAGCGGACCGGCGGAGCGGCTCTGGAACACAGGCCATC 408
QY 322 CAGTACCTTGGAGAGCGCTGCAAGAGATGGCGTCAAGCAGGATGTATCCAGCAGCC 381
Db 409 CTGCGCTGCTCAACCCGGTGGAGATGAACCGGACCGCAGGTGTTGCGGCGCCGCTC 468
QY 382 GCGGAGTGGTGGAGTCCACCGCGAGCAATTTGACTTNCACAA 428
Db 469 ACCTCGTGGAGTGTACACACCGAGTACCGAGGCCCTCTTGGGCAA 515

RESULT 6
US-09-902-540-907
; Sequence 907, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 907
; LENGTH: 6821
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:

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; NAME/KEY: unsure
; LOCATION: (1)..(6821)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-907

Query Match      7.6%; Score 45.2; DB 4; Length 6821;
Best Local Similarity 45.5%; Pred. No. 0.021;
Matches 158; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 82 GCGCGCGCAGAGCATGAAGCTGGCGGTTGACACCTTCTACGATAAGGTGCTGGCTGAC 141
Db 5097 GGGCTGCTCGCGCGGAGGCGCTGGCGACGTGCTGTTCCACGACAGCGGCCCTGTCAAGC 5156
QY 142 CCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGAGATCAAGAGAGAGATGAAGCAGGTC 201
Db 5157 TGGCGGACGGTGTCTCGCGAGTGCCTGCGGAGTGCCTGCGGAGGCGCTGACGCTGCCACCGCC 5216
QY 202 AAGTTTCATGAGCTTCTGTTGGCGGAGCAGACCATACAAAGGCGCCGAAAGCATGTAGCAC 261
Db 5217 AAGGCCAAGGGCTGCGACGAGCACCTGTCCGAGCGCAACCCGCCACCTGCTGAAAGCTG 5276
QY 262 GCACACGCCCATCTGTTCAAGGGCCACCGCTTGAGAGATCAAGGCGCCGAAAGCATCAAG 321
Db 5277 GCTTACAAACCGCTGTTTCATGTGGAGCGGACCGGCGGACCGGCTCTGGAACAGGCCATC 5336
QY 322 CAGTACCTTGGAGAGCGCTGCAAGAGATGGCGTCAAGCAGGATGTATCCAGCAGCC 381
Db 5337 CTGCGCTGCTCAACCCGGTGGAGATGAACCGGACCGCAGGTGTTGCGGCGCCGCTC 5396
QY 382 GCGGAGTGGTGGAGTCCACCGCGAGCAATTTGACTTNCACAA 428
Db 5397 ACCTCGTGGAGTGTACACACCGAGTACCGAGGCCCTCTTGGGCAA 5443

RESULT 7
US-09-902-540-14/c
; Sequence 14, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(603)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-14

Query Match      7.3%; Score 43.4; DB 4; Length 603;
Best Local Similarity 45.4%; Pred. No. 0.026;
Matches 152; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 30 CACAGACCGCGGAGCGGATCGCGGCGCAGAGACTGTTTCATGACCTTGGCGGCGC 89
Db 601 CGCAATATCCCGGCGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 542
QY 90 AGAAGGCATGAAGCTGGCGGTTGACACCTTCTACGATAAGGTGCTGACCCGAGACT 149
Db 541 GCTCAACCGCGGAGCTGCTCACCAGACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 482
QY 150 GCTGCCCTTCTTCGAGTCCCTGGACATGTCAAGAGCAGAGATGAAGCAGGTTCAAT 209

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Fri Feb 25 16:26:58 2005

481 TGGGCGCTTCGCAAGTACGTGGCGCGCTGGAGCTGGTGAAGATGCCGAGGTGCT 422
210 GAGCTTCGTGTTGGCGGAGCAGACCAATACAGGGCGGAAGCATGTACGACGACACGC 269
421 CGGACCGGTGAGGGCGCGAAATCATCAGCCAGGACTTACCGCGTGTTCGCCATGGACGC 362
270 CCATCTGTCAAGCGCCAGCGCTGGACCGCCACTTTGACAAGATCAAGCAGTACCT 329
361 CTTGTGGTGGCAGCAGCGCATGCGCGCTTCGACACGACAGCGGTGTTCTGGGAGGA 302
330 TCGAGAGACGCTGCAAGAGATGGCGTCAAGCAGG 364
301 GGGCCAGTTCCTCCGCGAGCGAGTCCGTGAGG 267

RESULT 8
US-09-902-540-5853
; Sequence 5853, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5853
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; NAME/KEY: unsure
; LOCATION: (1)..(603)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-5853

Query Match 7.3%; Score 43.4; DB 4; Length 603;
Best Local Similarity 45.4%; Pred. No. 0.026;
Matches 152; Conservative 0; Mismatches 183; Indels 0; Gaps 0;
QY 30 CACAGAGCGCGGAAGCGGATGCGGGCGCAAGAGCTGTTGATCACTGGCGGCGC 89
Db 3 CGAAATCCCGGNCGTGGTGGCGTGGACNCGGTGATGGTGGCCACTGACCTGCT 62
QY 90 AGAAGGCATGAAGCTGGCGTGTGACCTTTAGGATAAGTGTGCTGACCGGAGCT 149
Db 63 GCTCAACCGCGCGAGTGTCTACCGACCCCGCGGCGCAAGGTGTGCTCGGCATC 122
QY 150 GCTGCTCTTCGAGTCCCTGGACATGCAAGACGAGAAGATGAAGCAGTCAAGTTCAT 209
Db 123 TGGCGCTTCGCAAGTACGTGGCGCGTGGAGTGGTGAAGATGCCGAGGTGCT 182
QY 210 GAGCTTCGTGTTGGCGGAGCAGACCAATACAGGGCGGAAGCATGTACGACGACGC 269
Db 183 CGGACCGGTGAGGGCGCGGAATCATCAGCCAGGACTTACCGCGTGTTCGCCATGGACGC 242
QY 270 CCATCTGTCAAGCGCCAGCGCTGGACCGCCACTTTGACAAGATCAAGCAGTACCT 329
Db 243 CTTGTGGTGGCAGCAGCGCATGCGCGCTTCGCGCACGACAAAGCGTGTCTGGGAGGA 302
QY 330 TGGAGAGCGCTGCAAGAGATGGCGTCAAGCAGG 364
Db 303 GGGCCAGTTCCTCCGCGAGCGAGTCCGTGAGG 337

RESULT 9
US-09-902-540-3555

; Sequence 3555, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3555
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; NAME/KEY: unsure
; LOCATION: (1)..(19019)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-3555

Query Match 7.2%; Score 42.8; DB 4; Length 585;
Best Local Similarity 48.4%; Pred. No. 0.038;
Matches 119; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
QY 78 CTTGGCGCGCGCAAGAGCATGAAGCTGGCGTGTGACCTTCTAGGATAAGTGTGCGC 137
Db 18 CTTGGCGCATCGCGGCTGCTCCACCTGGGAGACGCGTCTTTCTGAGCGGATGCCAG 77
QY 138 TGACCGCGAGCTGCTGCCCTTCTTCAGTCCCTGGACATGCAAGACGAGAATGAAGCA 197
Db 78 CCAGGCGCAGATGCTGGCGAGCATCGAGAAGCTGGACAGAGAGAGGCCAGCAGACCA 137
QY 198 GGTCAAGTTCATGAGCTTCTGTTTGGCGGAGCAGACCAATACAGGGCGGAGCATGTA 257
Db 138 GGTCTGATCAGCAGTGGCGAGAGCGCGCGCGGAGACCGCGGAGCAGCAGCTACGATTG 197
QY 258 CGAGCGCAGCGCCATCTGTCAAGGGCCAGCGCTGGACCGCCACTTTTCAAGAT 317
Db 198 CTCTGCGCGAGCAGTGTGCTGGTGGCGAGCAGACCCCACTCCCGCGTGGAGAGCT 257
QY 318 CAAGCA 323
Db 258 CAAGCA 263

RESULT 10
US-09-902-540-1171
; Sequence 1171, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1171
; LENGTH: 19019
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; NAME/KEY: unsure
; LOCATION: (1)..(19019)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1171

Query Match 7.2%; Score 42.8; DB 4; Length 19019;
Best Local Similarity 48.4%; Pred. No. 0.14;

Matches 119; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

Qy 78 CTTGGGGGGGAGGAGGATGAAGCTGGCGTTGACACTTCTAGATAAGTGTGGC 137
 Db |||||
 9777 CGTGGCGATCGCGGGGTCTCCACTTGGAGACGGTCTCTTTCGAGCGGATGCCAG 9836
 Qy 138 TGACCCGGAGCTCTGCTCCCTTCTTCGAGTCCCTGGACATGCAAGACAGAGATGAAGCA 197
 Db |||||
 9837 CCAGGCGAGATCTGGCGAGCATCGAGAGCTGGACAGAGAGAGAGAGAGAGAGAG 9896
 Qy 198 GGTCAAGTTATGAGCTTGTGTTGGCGGAGCAGACCAATACAAAGCGCGAAGCATGTA 257
 Db |||||
 9897 GGCCTGCATCAGCAAGTGCAGAGAGCGCGCGCGGGAGCCCGCGAGGACAGCTACGATTG 9956
 Qy 258 CGAGCGACACGCCCATCTGTCTAAGGGCCAGCGCTGGACACCGCCACTTTTCACAAGAT 317
 Db |||||
 9957 CTCTGCGGAGAGTGCATGGGCTGCGAGCAGCCCACTCCCGCTCGGAGAGCT 10016
 Qy 318 CAAGCA 323
 Db |||||
 10017 CAAGCA 10022

RESULT 11
 US-09-744-072-1
 ; Sequence 1, Application US/09744072
 ; Patent No. 6823328
 ; GENERAL INFORMATION:
 ; APPLICANT: SCHERER, STEPHEN W.
 ; APPLICANT: MINASSIAN, BERGE A.
 ; APPLICANT: ROULEAU, GUY
 ; APPLICANT: DALGADO-ESCUETA, ANTONIO
 ; TITLE OF INVENTION: LAFORA'S DISEASE GENE
 ; FILE REFERENCE: 086671/0113
 ; CURRENT APPLICATION NUMBER: US/09/744,072
 ; CURRENT FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 60/093,495
 ; PRIOR FILING DATE: 1998-07-20
 ; PRIOR APPLICATION NUMBER: 60/130,269
 ; PRIOR FILING DATE: 1999-04-21
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 3128
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 US-09-744-072-1

Query Match 7.1%; Score 42.6; DB 4; Length 3128;
 Best Local Similarity 50.7%; Pred. No. 0.081;
 Matches 102; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Qy 1 GCGTGTCTGCGAGACGGCGCCACAGCACAGAGACGGCGAGCGGATGCGGGCGC 60
 Db |||||
 22 GTGGTCCACCGCGCGTGGCGCGCGCGCGCGCGCGTGTGTGTGGTGGCGCGCC 81
 Qy 61 AAGAGCTTTTATGACTTGGCGCGCGCGAGAGCATGAGTGGCGGTTGACACTTC 120
 Db |||||
 82 GAGTGGGGCGTTGGGAGCGCGCGCGTGTCCCTGAGCGCGCGCGCGCGCGCG 141
 Qy 121 TACGATAAGTGTGGTGTGACCGCGCGCGTGTGTCTTTCGAGTCCCTGGACATCAA 180
 Db |||||
 142 GCGACCGGGCCCTTGGCGTGCAGAGCGCGGGCTGTGGTTCGGGAGTGGAGTGGCG 201
 Qy 181 GAGCAGAGATGAAGCAGGTC 201
 Db |||||
 202 GCCGAGGAGCGCGCGCAGGAC 222

RESULT 12
 US-09-949-016-16800
 ; Sequence 16800, Application US/09949016
 ; Patent No. 6812339

GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16800
 ; LENGTH: 26896
 ; TYPE: DNA
 ; ORGANISM: Human
 ; ORGANISM: Human
 US-09-949-016-16800

Query Match 7.1%; Score 42.4; DB 4; Length 26896;
 Best Local Similarity 47.7%; Pred. No. 0.21;
 Matches 124; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

Qy 137 CTGACCCGGAGCTGTGCTCTTCTTCGAGTCCCTGACATGCAAGACAGAGATGAAGC 196
 Db |||||
 22334 CAGACCATGTGCACCTCTCTCTGCACACAGCGCCCATGATGGCAGAGGAGCTGAAGA 22393
 Qy 197 AGTCAAGTTATGAGCTTGTGTTGGGGGAGCAGACCAATACAAAGCGCGGAGCATGT 256
 Db |||||
 22394 AGGAGCAGGACACACAGCGCCCTGAGCGCATGAAGAAGAAACATGGAAACAGACCATTA 22453
 Qy 257 AGAGCGCACAGCGCCATCTGTCAGCGCCAGCGCTGAGACACCGCCACTTTTGACAAGA 316
 Db |||||
 22454 AGACCTGCAGCACCGGCTGGACGAAGCCGACAGATCGCCCTCAAGGGCGGCAAGAGC 22513
 Qy 317 TCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGC 376
 Db |||||
 22514 AGCTGCAGAGCTGGAAGCGCGGTGCGGAGCTGGAGATGAGCTGGAGGCGGAGCAGA 22573
 Qy 377 AGCGCCCGGAGTGTGGAG 396
 Db |||||
 22574 AGCGCAACGACAGATCGGTG 22593

RESULT 13
 US-09-252-991A-11092
 ; Sequence 11092, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 11092
 ; LENGTH: 759
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-11092

Query Match 7.1%; Score 42.2; DB 4; Length 759;
 Best Local Similarity 51.9%; Pred. No. 0.061;
 Matches 95; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 53 GCGGGCGCAAGAAGCTCTTTGATGACCTGGGCGGCGCAGAGGATGAAGTGGCGGTTG 112

Db 500 GCGACCGAAGTGGCTGCGCGGAGGCGCGAGGTGGCGAGCCGTACCTCGCGGTA 559
Qy 113 ACACCTTCTAGATAAGGTGCTGCGTGAACCGGAGTGTGCTCCCTTCTTGAGTCCCTGG 172
Db 560 CGCTCGCTGGGACGCGGAGTGGCTACTTCGACCTGCAACACGACTTTCGCGGCTGC 619
Qy 173 ACATCAAGAGCAGAAAGATGAAGAGGTCAAGTTCATGAGTTCGTGTTGGCGGACAG 232
Db 620 ATCGACACTGGAAGAGCTGGAGCAGGACCCGCGGCTCGCTTCGCCCATGCCATCGAGG 679
Qy 233 ACC 235
Db 680 ATC 682

RESULT 14
US-09-452-239-11
; Sequence 11, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeyol-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/1110,594
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 1058
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-452-239-11

Query Match 7.0%; Score 42; DB 3; Length 1058;
Best Local Similarity 52.9%; Pred. No. 0.079; Mismatches 80; Indels 0; Gaps 0;
Matches 90; Conservative 0;
Qy 162 CGAGTCCCTGGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTCATGAGCTTCGTGT 221
Db 619 CAACTACTCACTACCAAGAGCGGCTGATGAGTGTCAAGTTCGCGGCTCGTCGG 678
Qy 222 TGGCGGAGCAGACCAATAAAGGCGCAGAGCATGTACGACGACAGCCCATCTGTCMA 281
Db 679 CTACGACAAACACGCTCTGGAACGGCTCCGTGCTGCTCCCGCGAGCGCCCATGCGCAA 738
Qy 282 GGGCCACGGCTGGACCAAGCGACCTTGACAGATCAAGCATACCTTG 331
Db 739 GTACATCCGCTACTACCGGACTTCGTGCTGAGTCAACAGGCCCTCG 788

RESULT 15
US-09-902-540-8164
; Sequence 8164, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8164
; LENGTH: 969

; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8164
Query Match 7.0%; Score 41.6; DB 4; Length 969;
Best Local Similarity 43.9%; Pred. No. 0.098; Mismatches 225; Indels 0; Gaps 0;
Matches 176; Conservative 0;
Qy 21 CACCAGCACACAGAGACGCGGATGCGGGCGCAAGAGCTGTTTGTATGACCT 80
Db 402 CACACGCTGAGAGACGCTGACCCGGGACAGGTGCTGGAGTTGCTGGACGACTACTT 461
Qy 81 GGGCGGCGCAGAAAGGCATGAAGCTGGCGGTGACACTTCTACGATAAGTGTGCTGA 140
Db 462 CGGCAATGCGCCCATCATGTCATGCGCGGCCACGCGCATCGTGAACAAGTTCTTGGCGGA 521
Qy 141 CCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAAAGATGAAGCAGGT 200
Db 522 CGGGATGCTCGCTGCTGGGGCGTTCCGGATGCGCGGAGAACACCGCGAGCTGGCCAT 581
Qy 201 CAACTTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAGGGCGCGAAGCATGTACGA 260
Db 582 GCGGCGGCGCTCGACATGCGCGCAAGCTGGAGGACATCAACGCCAGCGCTGCAGCG 641
Qy 261 CGCACACGCGCATCTGTGTCAGGGCGCACGGCTGGACCCAGCCGCACTTTCACAGATCAA 320
Db 642 AGGTCTCGCGCGCTGCGCATCGGCTCGGCTGCAACCGGCGATGGTGGCGGCGGCGAT 701
Qy 321 GCAGTACTTGGAGAGACGCTGCAAGAGATGGGCGTCAAGCAGGATGTGATCCAGCACGC 380
Db 702 GCTCGGCGGCGCGAGCAGCAGGTACCGGTACCGTATCGGTGACGCGTGAACCTGGCGTC 761
Qy 381 CGCGGAGTGTGAGTCCACCGCGCAGAAATTTGACTTNC 421
Db 762 TCGGTGAGGGCCCTCACCAAGTCCCGCGGTGGACATCC 802
Search completed: February 22, 2005, 21:14:40
Job time : 122 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2005, 20:25:43 ; Search time 402 Seconds
(without alignments)
8792.231 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 598

Sequence: 1 ggcgtgcctgcagacgcgc.....agccatttcgaccaaagcc 598

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5384158 seqs; 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74.4	12.4	372	17	US-10-282-122A-25335
2	50	8.4	2466	15	US-10-156-761-5788
3	50	8.4	9025608	15	US-10-156-761-1
4	47.6	8.0	2256646	18	US-10-470-565-1
5	47.4	7.9	548	18	US-10-437-963-94550
6	46.6	7.8	1389	18	US-10-411-910A-255
7	46.6	7.8	1389	18	US-10-411-910A-257
8	46.2	7.7	1209	17	US-10-369-493-32038
9	46.2	7.7	1509	18	US-10-411-910A-264
10	45.8	7.7	2209	18	US-10-437-963-69229
11	45.2	7.6	2238	18	US-10-437-963-97363

12	44.4	7.4	1445	18	US-10-437-963-35783
13	44.2	7.4	1000	17	US-10-389-566-49
14	44.2	7.4	1377	17	US-10-369-493-39791
15	44.2	7.4	1395	17	US-10-369-493-39403
16	44.2	7.4	1404	17	US-10-369-493-39036
17	44.2	7.4	2055	17	US-10-389-566-235
18	44	7.4	1368	18	US-10-437-963-7459
19	43.8	7.3	1507	18	US-10-425-115-108376
20	43.8	7.3	2278	18	US-10-739-930-4715
21	43	7.2	681	18	US-10-767-701-23705
22	42.8	7.2	2645	18	US-10-437-963-95877
23	42.6	7.1	1403	15	US-10-156-761-4532
24	42.6	7.1	2121	15	US-10-755-889-419
25	42.6	7.1	3128	18	US-10-156-761-2429
26	42.6	7.1	9025608	15	US-10-886-033-1
27	42.6	7.1	932	18	US-10-156-761-1
28	42.4	7.1	25000	11	US-09-968-007A-215
29	42.4	7.1	1055	18	US-10-437-963-4170
30	42.2	7.0	1058	9	US-09-452-239-11
31	42	7.0	1483	18	US-10-437-963-33390
32	42	7.0	1060	18	US-10-437-963-62449
33	42	7.0	1425	17	US-10-354-437-31
34	41.8	7.0	1280	9	US-09-923-922-4
35	41.6	7.0	1280	9	US-09-954-456-1590
36	41.6	7.0	1280	17	US-10-390-553-4
37	41.6	7.0	1817	9	US-09-924-417-64
38	41.6	7.0	1817	14	US-10-067-741-45
39	41.6	7.0	1817	17	US-10-653-872-64
40	41.6	7.0	2887	15	US-10-327-805-1
41	41.6	7.0	2967	17	US-10-282-122A-14992
42	41.6	7.0	3083	9	US-09-371-900-36
43	41.6	7.0	3083	9	US-09-924-417-62
44	41.6	7.0	3083	9	US-09-970-820-36
45	41.6	7.0	3083	9	US-09-970-820-36

ALIGNMENTS

RESULT 1
US-10-282-122A-25335
Sequence 25335, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625

Sequence 35783, A
Sequence 49, Appl
Sequence 39791, A
Sequence 39403, A
Sequence 39036, A
Sequence 235, App
Sequence 7459, Ap
Sequence 108376,
Sequence 4715, Ap
Sequence 23705, A
Sequence 95877, A
Sequence 4532, Ap
Sequence 419, App
Sequence 2429, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 5556, Ap
Sequence 215, App
Sequence 4170, Ap
Sequence 11, Appl
Sequence 62449, A
Sequence 33390, A
Sequence 31, Appl
Sequence 4, Appli
Sequence 1590, Ap
Sequence 4, Appli
Sequence 64, Appl
Sequence 45, Appl
Sequence 64, Appl
Sequence 1, Appli
Sequence 14992, A
Sequence 36, Appl
Sequence 62, Appl
Sequence 36, Appl

	Query Match	8.4%;	Score 50;	DB 15;	Length 2466;
	Best Local Similarity	47.1%;	Pred. No. 4.6e-05;		
	Matches 152;	Conservative	0;	Mismatches 171;	Indels 0; Gaps 0;
QY	115	ACCTTCTACGATAAGGTGCTGGCTGACCCGAGGTGTCGCCCTTCTTCGAGTCCTCGAC	174		
Db	421	ACCTCCCACTGCTGCTGCCGAGACCCGCGCTGCTGGCGGCGACGGCCCGCTGGTC	480		
QY	175	ATGCAAGAGCAGAAGATGAACAGGTCAAGTTCAAGAGCTTCGTGTTTGGCGGAGCAGAC	234		
Db	481	CTGTGTCGACGACGAGTTCTCCACCGCAACACGGTCTCTCAACACCATCCGCGACCTGCAC	540		
QY	235	CAATACAGGGCGCGAAGCATGTACAGCGCACACGCCCATCTGGTCAAGGGSCACGGCGTG	294		
Db	541	GAGCGCTATCGCGCGCGCGGTACGTGTCGTGCCCTCGTGGACATGCGCTCCCCGGCC	600		
QY	295	GACCACCGCCACTTTGACAAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGATGGGC	354		
Db	601	GACCTCGGGCGCTGGACGATTCGGCGCGAGATCGTGCCCGGTGGACCTGATCACG	660		
QY	355	GTCAGACAGGATGTGATCCAGCACGCCCGCGAGTGTGGAGTCCACCCGCGACGAATTT	414		
Db	661	GCCCGCTCGGGACGGTGAAGTGTCCCGAGGGCGTGTGGAGAAGGGGACAGGAGTGGTC	720		
QY	415	GACTTNCACAACTGCGCAC	437		
Db	721	GCCCGGCACGAGAGGGCGGTACC	743		

	Query Match	8.4%	Score 50	DB 15	Length 9025608
	Best Local Similarity	47.1%	Pred. No. 0.00058		
	Matches 152	Conservative	0	Mismatches 171	Indels 0
	Gaps				
Qy	115	ACTTTCTACATTAAGGTGCTGTGACCCGGAGCTGCTCCCTTCTTCGAGTGCCTTGGAC	174		
Db	7015347	ACCTCCACACCTGTGTGTCGCCGAGGACCCGGCGCTGCTGGCGGCGACCGCCCGCTGGTC	7015406		
Qy	175	ATGCAACAGCAGCAAGATGAACAGGCTCAAGTTCATGAGCTTCGTGTTTCGCGAGCAGAC	234		
Db	7015407	CTGTCGACGACGAGTTCTCCACGGCGAACACGGTCCTCAACACCATCGCGACCTTGCAC	7015466		

```

RESULT 2
US/10-156-761-5788
Sequence 5788, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBEA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 5788
LENGTH: 2466
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1) .. (2466)

```


RESULT 4

8

RESULT

	Query Match	7.8%	Score 46.6	DB 18	Length 1389
	Best Local Similarity	44.9%	Pred. No. 0.00046		
	Matches 175	Conservative	0	Mismatches 215	Indels 0
Qy	40	CGCGAAGCGGATCGGCGCGAAGAGCTGTTTATGACTGGCGCGCGCGAGAGCGCATG	99		
Db	685	GTGTGTGTGGCCCCCTGCTACGACAAGAAGCTGGAGGCCCTGCGCGAGGGCGCTGAGCACCC	744		
Oy	100	AAGCTGGCGGTGACACCTTCTACGATAAGTGTGGTCTGACCCCGAGACTGCTGCGCCCTTC	159		

Db 745 ACCCTGAACGGCGCCGCGGACCGACCTGCTGTGACACGCGGAGATCGCCACGATC 804
 Qy 160 TTCGAGTCCCTGGACATCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTG 219
 Db 805 ATGGAGCAGAGCGACTGAGCGTGAGACATCGCGTGGACACCTGTTGCGGACATG 864
 Qy 220 TTTCGCGGAGCAGACCAATACAAGGGCCGAAGCATGTACGACGACACGCCCATCTTGCTC 279
 Db 865 AAGGAGGTGGCGTGCAGCGCCACGACGCGTGTAGCAGCAGCGCCACCTGGCCACGTTG 924
 Qy 280 AAGGCGCAGCGCTGGACACCGCCACTTTCACAGATCAAGCAGTACCTTGGAGAGCG 339
 Db 925 TTTCGCCACGCGCCGCAAGAGCTGTTCGCGGAGACGCTGGAGGAGATCACCTACCGCGCC 984
 Qy 340 CTGCAAGATGGCGGTCAAGCAGATGTGATCCAGCAGCGCGCGGAGTGTGGAGTCC 399
 Db 985 CTGCGCAACAGAGCTTTCACAGGTGACCTTGGAGAGAGCGGAGGTGCTGCTGCGC 1044
 Qy 400 ACCCGCAGCAATTTGACTTNNCCCAAC 429
 Db 1045 TTTCGCCGCGCTACGGCTTCGCAACATC 1074

RESULT 7
 US-10-411-910A-257
 ; Sequence 257, Application US/10411910A
 ; Publication No. US20040209256A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Harrison F.
 ; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
 ; FILE REFERENCE: H2041203-P
 ; CURRENT APPLICATION NUMBER: US/10/411,910A
 ; CURRENT FILING DATE: 2003-04-12
 ; NUMBER OF SEQ ID NOS: 343
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 257
 ; LENGTH: 1389
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-411-910A-257

Query Match 7.8%; Score 46.6; DB 18; Length 1389;
 Best Local Similarity 44.9%; Pred. No. 0.00046;
 Matches 175; Conservative 0; Mismatches 215; Indels 0; Gaps 0;
 Qy 40 GCGGAAGCGGATGCGCGCGCAAGAGCTGTTTGATGACCTGGCGCGCAGAGCATG 99
 Db 685 GTGGTGTGCCCCCTGTACGACAGAGAGCTGGAGGCGCTGCGGAGGCGCTGAGCACC 744
 Qy 100 AAGTGGCGGTTGACACCTTCTACGATAGGTGCTGCTGACCGGAGCTGCTGCTTC 159
 Db 745 ACCCTGAACGCGCGCGCGCACCGACTGCTGCTGCTGACCGGCGGAGATCGCCAGATC 804
 Qy 160 TTGAGTCCCTGACATGCAAGAGCAGAGATGAAGCAGTCAAGTTTCATGAGCTTCGTG 219
 Db 805 ATGAGCAGAGCAGCTTACCGTGAAGGACATCGCGTGGACACCTGTTGCGGACATG 864
 Qy 220 TTTCGCGGAGCAGACCAATACAAGGGCCGAAGCATGTACAGCAGCAGCCCATCTGGTTC 279
 Db 865 AAGGAGTGGCGTGTGACGCGCCACGACGCGGCTGAGCAGCAGCCACCTGGCCACGTTG 924
 Qy 280 AAGGCCACGCGCTGGACACCGCCACTTTGACAGATCAAGCAGTACCTTGGAGAGAGC 339
 Db 925 TTTCGCCACGCGCCGCAAGAGCTGTTTCGCGGAGACGCTGGAGGAGATCACCTACCGCGCC 984
 Qy 340 CTGCAAGATGGCGGTCAAGCAGAGATGTATCCAGCAGCGCGCGGAGTGTGGAGTCC 399
 Db 985 CTGCGCAACAGAGCTTTCACAGGTGACCTTGGAGAGAGAGCGGAGGTGCTGCTGCGC 1044
 Qy 400 ACCCGCAGCAATTTGACTTNNCCCAAC 429
 Db 1045 TTTCGCCGCGCTACGGCTTCGCAACATC 1074

RESULT 8
 US-10-369-493-32038
 ; Sequence 32038, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 32038
 ; LENGTH: 1209
 ; TYPE: DNA
 ; ORGANISM: Thermobifida fusca
 US-10-369-493-32038

Query Match 7.7%; Score 46.2; DB 17; Length 1209;
 Best Local Similarity 55.2%; Pred. No. 0.00059;
 Matches 90; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Qy 248 GAACCATGTACGACGACACGCGCCATCTGTCAAGGCGCCACGCGCTGGACACCGCCACT 307
 Db 86 GCACCTCTGCTTTCGACGAAGTGTGTGGTGGAGCGCGCCGCGAGGACGACCTGT 145
 Qy 308 TTGACAAGATCAAGCAGTACCTTGGAGAGAGCTGCAAGAGATGGCGTCAAGCAGATG 367
 Db 146 TCGTCCAGCTCTGCGGACCGGGGGTGCCTGTCATGAATTCGGCAGCTGCTCGCG 205
 Qy 368 TGATCCAGACGCGCGCGGAGTGTGTGAGTCCACCCCGCAGCA 410
 Db 206 AGACTCTGCATCCCCGAGGAGAGAGTTCATCTTCGACGA 248

RESULT 9
 US-10-411-910A-264
 ; Sequence 264, Application US/10411910A
 ; Publication No. US20040209256A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Harrison F.
 ; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
 ; FILE REFERENCE: H2041203-P
 ; CURRENT APPLICATION NUMBER: US/10/411,910A
 ; CURRENT FILING DATE: 2003-04-12
 ; NUMBER OF SEQ ID NOS: 343
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 264
 ; LENGTH: 1509
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-411-910A-264

Query Match 7.7%; Score 46.2; DB 18; Length 1509;
 Best Local Similarity 46.2%; Pred. No. 0.00064;
 Matches 153; Conservative 0; Mismatches 178; Indels 0; Gaps 0;
 Qy 54 CGGCGCAGAGAGCTGTTGATGACCTGGCGCGCAGAGCATGAAGCTGGCGGTGA 113
 Db 846 CGGCGCGAGCGCGCTTGCAGCGCGCAAGATCGCCCCCTGACAGACCTGGCGCGCG 905
 Qy 114 CACCTTCTACGATGAAGTGTGCTGACCGGAGCTGTGCGCTTCTTCGAGTCCCTGA 173
 Db 906 CGGCGGAGATCGCCACAGATCATGAGCAGGCGGACCTGAGCGTGGCGGCGCGCGTGA 965

QY 174 CATCAAGAGCAGAGTGAAGTCAAGTCAAGTTCATGAGCTTCGTTGTTGGCGGAGCAGA 233
Db 966 CACCTTGTTCGGGACCTGAGAGGAGCAGAGTGTACCCGCCACGCGGCCAGCAGCGA 1025
QY 234 CCAATACAAAGGCGGAGCATGTACGACGACGCCCCATCTGGTCAAGGGCCACGGCTT 293
Db 1026 CGGCCACTTGGCCACATCTTCGCCACGCGCCCAAGGAGCTGTTCACAGGAGCAGTGA 1085
QY 294 GGACACCCGCACTTTGACAAGTCAAGCAGTACCTTGGAGAGAGCGCTCAAGAGATGG 353
Db 1086 GGAGGTGACCTACCGCGCCCTCGCAACAAGGACTTCCAGGAGGTACCCCTGGAGAGAA 1145
QY 354 CGTCAAGCAGAGTGTATCCAGCAGCGCCGCC 384
Db 1146 CGCGAGGTGTCTCGCTTCGCTTCGCCGCCGCC 1176

RESULT 10
US-10-437-963-69229
; Sequence 69229, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 69229
; LENGTH: 2209
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_69918C.1
US-10-437-963-69229

Query Match 7.7%; Score 45.8; DB 18; Length 2209;
Best Local Similarity 46.1%; Pred. No. 0.00096;
Matches 152; Conservative 0; Mismatches 178; Indels 0; Gaps 0;
QY 110 TTGACACCTCTACGATAAGTGTCTGGCTCACCGGAGTGTCTGCCCTTCTTCGAGTCCC 169
Db 400 TCGACTACGTGTGTCTCAAGCGGACCGACCGGAGCTCCCGGAGCTGTGGCGG 459
QY 170 TGGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAG 229
Db 460 AGATCATCCAGCGGAACAAGCTGTCTGGGCTGGAGGAGTCAAGTTCTCTCTCAAGGTCA 519
QY 230 CAGACCAATACAAAGGCGGAGCATGTACGACGACACGCCCTCTGGTCAAGGGCCACG 289
Db 520 TCGTCAACTCCGGCATCCGGGAGGAGACCTACGGGCCCGGAAACATCATCGCGGGCGG 579
QY 290 GCCTGGACACCGCCACTTTGACAAGATCAAGCAGTACCTTGGAGAGACCTGCAAGAGA 349
Db 580 ACGCCGCCCGGACCGGCTCGCCGAGGGGATGGAGGAGATGGACGAGACGTTCACGCCG 639
QY 350 TGGCGGTCAAGCAGGATGTATCCAGCAGCAGCGCGGAGTGGTGGAGTCCACCGCGCAGC 409
Db 640 TGCTCAGCAGCTGTTTCGCGGCTCTGTCGCGGGCGGGCGGGCGGTCCGCCCGCG 699
QY 410 AATTGACTTNCACAACTGCGCACCCA 439
Db 700 ACGTCGACCTCTCGTCTCAACGTGTCCA 729

RESULT 11
US-10-437-963-97363/c
; Sequence 97363, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 97363
; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95374C.1
US-10-437-963-97363

Query Match 7.6%; Score 45.2; DB 18; Length 2238;
Best Local Similarity 50.2%; Pred. No. 0.0015;
Matches 110; Conservative 0; Mismatches 109; Indels 0; Gaps 0;
QY 216 CGTGTTCGCGGAGCAGCAATACAAAGGCGGAGCATGTACGACGACACGCCCATCT 275
Db 1249 CGTGTTCGCGGCTGCGACGCGCGCTCGCGCCATCTTCGTGACCTCGCCGCTG 1190
QY 276 GGTCAAGGCGCAGCGCTTGACCCACCGCCACTTTGACAGATCAAGCAGTACCTTGAGA 335
Db 1189 CGCATGCTCCAGATGCTCAACTTACCGAGGCGGTGCGCATGACGAAGCGCCGCCGA 1130
QY 336 GAGCGTCAAGAGATGGCGTCAAGCAGGATGTATCCAGCAGCGCGCGAGTGGTGA 395
Db 1129 GAAGCTCTTCAAGGTGCTCGACATGTACGAGGCGGTCCGCGACGCGCCCGCTCATCGA 1070
QY 396 GTCCACCGCGCAGAAATTTGACTTNCCTCAACTGCGC 434
Db 1069 CGCTTCATCGCGCTGCTCCACCGAGCGCGCGC 1031

RESULT 12
US-10-437-963-35783
; Sequence 35783, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 35783
; LENGTH: 1445
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39672C.1

US-10-437-963-35783

Query Match 7.4%; Score 44.4; DB 18; Length 1445;
Best Local Similarity 46.5%; Pred. No. 0.0023;
Matches 141; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 139 GACCCGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATCAAGAGCAGAAAGATGAAGCAG 198
|||
Db 167 GACCGCTCGAGCTGCGCCAGACCTCGACCGGAGCTCGCGAGCTCGAGCCCAAGCTG 226
|||
QY 199 GTCAAGTTCATGAGCTTCGTGTTTGGCGAGCAGACCAATACAAGGGCCGCAAGCATGTAC 258
|||
Db 227 GCCCAGCTGCCCGCCGCGGCAACCCGCGCTGCTCCAGTGCACGCCGTGTACGAGGAC 286
|||
QY 259 GAGCAGACGCCATCTGCTCAAGGCCACGCGCTGGACACCGCCACTTTCACAGATC 318
|||
Db 287 GAGCGGTGACGCACATGCTATGACCTCTCTCCGCGCCGAGCTGCTCGACTGGATC 346
|||
QY 319 AAGCAGTACTTTGGAGAGACGCTGCAAGAGATGGCGTCAAGCAGGATGTATCCAGCAC 378
|||
Db 347 CGCTCCGCGCGCGCGCGCTCCCGAGCCCGTCCGCGCGCGCTGCTCGCGAGCTC 406
|||
QY 379 GCGCGGAGTGGTGAAGTCCACCGCGACGAAATTGACTTNCACAACTGCGCACCC 438
|||
Db 407 GCGGAGGCGCTCGCGCACTGCCACCGCGCGGGTCCGCCACCGGACGTCAAGCCCGAC 466
|||
QY 439 AAC 441
|||
Db 467 AAC 469

RESULT 13

US-10-389-566-49/c
; Sequence 49, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Zea mays
US-10-389-566-49

Query Match 7.4%; Score 44.2; DB 17; Length 1000;
Best Local Similarity 53.8%; Pred. No. 0.0024;
Matches 91; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 66 GCTGTTTATGACCTGGCGCGCCAGAGGATGAAGCTGGCGGTGACACCTTCTACGA 125
|||
Db 676 GCAGTTTCATCGCGCGGTCCACGCGCGCGAGATGCTCACGGTAGAGGGCTACACGA 617
|||
QY 126 TAAGTGTGGTGAACCGGAGCTGCTGCTTCTTCGAGTCCCTGGACATGCAAGACA 185
|||
Db 616 CATCTGTCGTCGCGAGGCAACCGCTGTCCGCGCGGAGATCTCTGGGTGACCGCCCC 557
|||
QY 186 GAAAGATGAAGCAGGTCAAGTTCATGAGTTCGTGTTTGGCGGAGCAGAC 234
|||
Db 556 GACGCTCAAGAGTCGAGGAGGTGGCGCGCTGCTGTTCTGTCGCGAC 508
|||

RESULT 14

US-10-369-493-39791
; Sequence 39791, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 39791
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-10-369-493-39791

Query Match 7.4%; Score 44.2; DB 17; Length 1377;
Best Local Similarity 48.2%; Pred. No. 0.0027;
Matches 124; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 151 CTGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAAAGATGAAGCTCAAGTTTATG 210
|||
Db 784 CTGGCCCGCTAGGTTGGTTCGATGGCGACAGGAGCTTTCAGCCAGCAGGAGTTGCTG 843
|||
QY 211 AGCTTCGTTTGGCGGAGCAGACCAATACAAAGGCCCAAGCATGTACGACACACGCC 270
|||
Db 844 GACCTGTTTCGACGTCAGGACGTCAATTCGAAGGCCGCGCTGGACATGCGCCAAAGCTC 903
|||
QY 271 CATCTGTCGAAGGCCGCGCTGGACCAACCGCCACTTTTGACAAGATCAAGCAGTACCTT 330
|||
Db 904 GGCTGGGTGATCAGCATTAATTGAAGACCGCAGCCGCGCAGCATCGCGCCGAGCTG 963
|||
QY 331 GGAGAGACGCTGCAAGAGATGGCGTCAAGCAGAGATGTATCCAGCAGCGCCGCGAGTG 390
|||
Db 964 GAATACCAAGCTCCGCAAGCTGGGATGATGTGGCCGCGCCGCGCTGCGCATGTG 1023
|||
QY 391 GTGGAGTCCACCCGCGA 407
|||
Db 1024 GTGGTGGCGCTGCGCGA 1040
|||

RESULT 15

US-10-369-493-39403
; Sequence 39403, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 39403
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-10-369-493-39403

Fri Feb 25 16:26:58 2005

Query Match 7.4%; Score 44.2; DB 17; Length 1395;
Best Local Similarity 48.2%; Pred. No. 0.0027;
Matches 124; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

Qy	151	CTGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATG	210
Db	793	CTGGCCCGCTAGGTTGGTCGATGGCGACCAAGAGCTGTTTCAGCCAGCAGGAGTTGCTG	852
Qy	211	AGCTTCGTGTTTGGCGGAGCAGACCAATACAAAGGGCCGAAGCATGTACGACGCACACGCC	270
Db	853	GACCTGTTTCGAGTCAAGGACGTCATTCGAAGGCCCGCGCTTGACATGGCCAAAGCTC	912
Qy	271	CATCTGCTCAAGGGCCACCGCCTGGACACCGCCACTTTGACAAGATCAAGCAGTACCTT	330
Db	913	GGCTGGGTGAATCAGCATTAATTGAAGACCGACCGCCCGCAGCATCGCGCCAGCTG	972
Qy	331	GGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGCAGCCGCCCGGAGTG	390
Db	973	GAATACCAAGCTCCGCAAGCTGGGCATTGATGTGGCCGCCGCCCGCCGCTGCCGATGTG	1032
Qy	391	GTGGAGTCCACCCGCGA	407
Db	1033	GTGGTGGCGCTGCGCGA	1049

Search completed: February 22, 2005, 21:21:44
Job time : 425 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 22, 2005, 21:02:19 ; Search time 31 Seconds

(without alignments)

2880.009 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 1067

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USER=US09920953@cgn_1_1_33@runat_17022005_103111_6324 -NCPU=6 -ICPU=3
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	136	12.1	345	4	US-09-252-991A-32377
C 3	134.5	12.0	170	4	US-09-252-991A-19980
C 4	134	11.9	663	4	US-09-252-991A-30843
C 5	130.5	11.6	308	4	US-09-252-991A-27249
C 6	129	12.1	1476	4	US-09-252-991A-29427
C 7	126	11.2	235	4	US-09-252-991A-24046
C 8	125.5	11.8	394	4	US-09-252-991A-19344
C 9	124	11.6	312	4	US-09-252-991A-19787
C 10	122	11.4	726	4	US-09-252-991A-20675
C 11	121.5	11.4	204	4	US-09-252-991A-17837
C 12	121.5	11.4	351	4	US-09-252-991A-18476

13	121	11.3	248	4	US-09-252-991A-20161	Sequence 20161, A
14	121	11.3	686	4	US-09-252-991A-20509	Sequence 20509, A
C 15	120	10.7	219	4	US-09-252-991A-23215	Sequence 23215, A
C 16	119.5	10.7	209	4	US-09-252-991A-24725	Sequence 24725, A
C 17	119.5	11.2	266	4	US-09-252-991A-32478	Sequence 32478, A
C 18	119.5	11.2	720	4	US-09-252-991A-32006	Sequence 32006, A
C 19	119	11.2	222	4	US-09-252-991A-26487	Sequence 26487, A
C 20	118.5	10.6	247	4	US-09-252-991A-26899	Sequence 26899, A
C 21	118	11.1	536	4	US-09-252-991A-20771	Sequence 20771, A
C 22	118	11.1	565	4	US-09-252-991A-20122	Sequence 20122, A
C 23	117.5	11.0	273	4	US-09-252-991A-30433	Sequence 30433, A
C 24	117	11.0	153	4	US-09-252-991A-20543	Sequence 20543, A
C 25	117	11.0	204	4	US-09-252-991A-21783	Sequence 21783, A
C 26	116.5	10.4	191	4	US-09-252-991A-25365	Sequence 25365, A
C 27	116.5	10.9	326	4	US-09-252-991A-18751	Sequence 18751, A
C 28	116.5	10.4	335	4	US-09-252-991A-23674	Sequence 23674, A
C 29	116.5	10.9	977	4	US-09-252-991A-16655	Sequence 16655, A
C 30	116	10.3	160	4	US-09-252-991A-30765	Sequence 30765, A
C 31	116	10.9	297	4	US-09-252-991A-28217	Sequence 28217, A
C 32	116	10.9	369	4	US-09-252-991A-20790	Sequence 20790, A
C 33	115.5	10.8	172	4	US-09-252-991A-20172	Sequence 20172, A
C 34	115	10.8	266	4	US-09-252-991A-19128	Sequence 19128, A
C 35	115	10.8	681	4	US-09-252-991A-21837	Sequence 21837, A
C 36	114.5	10.7	143	4	US-09-252-991A-25813	Sequence 25813, A
C 37	114.5	10.7	168	4	US-09-252-991A-23614	Sequence 23614, A
C 38	114.5	10.2	173	4	US-09-252-991A-33359	Sequence 33359, A
C 39	114.5	10.2	200	4	US-09-252-991A-24828	Sequence 24828, A
C 40	114.5	10.7	474	4	US-09-252-991A-16788	Sequence 16788, A
C 41	114	10.7	320	4	US-09-252-991A-24634	Sequence 24634, A
C 42	114	10.7	480	4	US-09-252-991A-31470	Sequence 31470, A
C 43	114	10.2	554	4	US-09-252-991A-28232	Sequence 28232, A
C 44	114	10.7	697	4	US-09-252-991A-24009	Sequence 24009, A
C 45	114	10.7	1706	4	US-09-252-991A-31760	Sequence 31760, A

ALIGNMENTS

RESULT 1

US-09-902-540-13031
; Sequence 13031, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B US/09/902,540
; CURRENT APPLICATION NUMBER: 2001-07-10
; PRIOR FILING DATE: 2001-07-10
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13031
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13031

Alignment Scores:	3.24e-16	Length:	126
Pred. No.:	232.00	Matches:	51
Score:	56.10%	Conservative:	18
Best Local Similarity:	41.46%	Mismatches:	48
Query Match:	21.74%	Indels:	6
DB:	4	Gaps:	2

US-09-920-953-2 (1-598) x US-09-902-540-13031 (1-126)

Qy 37 ACGCCGAAGCGGATCGCGCGCAAGAGCTGTTTGTATGACCTGGCGCGCAGAGGCC 96

Db 4 ThrAlaGlu-----LysSerValTyrGluInLeuGlyGlyGluProAla 18

QY	539	CAGGCTCTGTGGCCCGCTTGGCGCGCTCGGCAACTGGCGTCCCC--GTCATAAATCGA	483
Dd	101	GlnGlyProGlyGlyProGlyArgAspArgGlnValArgLeuProAlaAlaProGlyArg	120
QY	482	TGGAATGAGCGCTCAGGCTGGGGTTGGGTTAAACAAAATCAGTTGGGTGCCAGTCTGTG	423
Dd	121	ProSerArgA-Ggin-::: -----SerArgLeu	128
QY	422	GGNAAGTCAAATTCTGTGCGGGTGACTCCACCACCTCGGCGGGTGCTGTA-----	371
Dd	129	GlnArgHisGlyLeuSerArgCysProLeu-ProLeuArgArgArgProSerProAla	148
QY	370	-----TCATCATCC	363
Dd	148	aTrpArgGlnPropColleGluLeuGlyAlaValArgLeuArgPropProGlnArgArgPr	168
QY	303	TCATCATCC	303

US-09-920-953-2 (1-598) x US-09-252-991A-19980 (1-170)

QY	524	CCTGGCGCGCTCGGCAACTGGCGCTCCCGCTCAA-----AATCGATGAATAGCGGC	471
		::::	::::
Db	14	ProGlyArgAsnArgAlaAlaProAlaAlaAlaGlyArgArgSerAlaArg	33
		::::	::::
QY	470	TCAGCTGG-----GGTTGGTTAATCAAAATCAGTTGGTGCGCAGTTGTGGGNAAG	417
		::::	::::
Db	34	SerGlyTrpProCysGlyTrp-----Arg-TrpSerHisProCysTrp	47
		::::	::::
QY	416	TCAAATTCTGTCGGGTGGACTCCACCACCTCCGGCGCGTGCTGTGGATTCACATTCCTGCTTG	357
		::::	::::

Db 48 -GlnHisArgArgArgProArgProSerArgArg-----SerArgProAlaAla 64
QY 356 AGCCCATCTCTTGAGCGCTCTCCAGGTTACTGTTGATCTTCTCAAGTGGCGGTGG 297
Db 64 aArgPro-----SerGlyGlyAla 70
QY 296 TCCAGCGCGTGGCCCTTGACACAGAT-----GGCGGTGGCGTGCATGCTTCGG 246
Db 70 aAlaIleArgArgProValProHisGlyGlnProGlyArgArgAsnAlaCys----- 88
QY 245 CCCTTGATTGTTGCTCGCCAAACACAGAGCTCATGAACTTGACCTGCTTCATCTC 186
Db 89 -----SerThrArg----- 91
QY 185 TGCTCTTGATGTCAGGAGCTCGA-----AGAAGGCGAGCAGC 147
Db 92 -----LeuProGlyArgArgArgPheProTrpArgProThrArgArgSerAla 108
QY 146 TCCGGGTGAG-----CCAGCACCTTATCGTAGA-----AG 117
Db 108 aProGlySerArgThrGluArgAlaProSerProAlaArgArgGlySerArgArgSerAr 128
QY 116 GTGTCAACCGCCAGCTTCATGCTTCTGCGCCCGCCAGGTGCATCAACAGCTTCTTGGCG 57
Db 128 gArgArgProAlaAla-----ArgArgGlyThrLeuProCysProAlaCysSe 144
QY 56 CGCATCCGCTTCCGC-----CGTCTCTGT-----GGTGTGTCGCGCGTCTGC 10
Db 144 r-AlaSerArgAsnArgSerArgSerCysSerArgSerGlySerAlaGlyArgSerCys 163

RESULT 4

US-09-252-991A-30843
; Sequence 30843, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30843
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30843

Alignment Scores:
Pred. No.: 1,62e-05 Length: 663
Score: 134.00 Matches: 53
Percent Similarity: 35.71% Conservative: 17
Best Local Similarity: 27.04% Mismatches: 71
Query Match: 11.94% Indels: 55
DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-30843 (1-663)

QY 512 CGGCAACTGGCGTCCCGCTCAAAATCGATGG-----AAT 477
Db 45 ArgArgValProIleArgCysAlaAsnAlaTrpProGlyArgProMetSerThrSer 64
QY 476 GAGCGCTCGCTGGGT-----TGGTTAAAGAAAT 444
Db 65 ArgArgProGlyTrpSerProAlaValProAlaGlyAlaCysCysTrpLysThrArgAsn 84
QY 443 CAGTTGGTGGCAGTGTGGGNAAGTCAAAATTCGTCGCGGTGAGCTCCACCACTCCG 384
Db 85 ValAlaGlyArgSerAlaThrAspAlaTrpSerSer-----AlaProAlaPro 100

QY 383 GCGCGTCTGATCACAATCCTGCTTGTAGCGCCCATCTCT-----TGCAGCGTCTCT 333
Db 101 AlaAsnCys-----CysCysLeuPheProAlaGlyProSerProAlaSerProAla 117
QY 332 CCAAGGTACTGCTTGTATCTTGTCAAGTGGCGGTGTCAGGCGC-----TGGCCC 282
Db 118 ProAlaAlaCysArg-----ArgTrpProArgAlaAlaCysHisTrpPro 132
QY 281 TTGACCAGATGGCGCTGTGCTGTCATGCTTCCGCCC-----TTGTATTGCTGCTGT 228
Db 133 AlaSerAlaTrp-----TrpTrpLeuAlaProAlaArgCysCysTrpProAla 148
QY 227 CGGCAAAACACAGACTCATGAACTTGACCTGCTTCACTTCTGCTTTCATGCTCCAGG 168
Db 149 ProPro-Ala-----ProAlaSerAlaGlyArgAlaCysCysAlaSe 162
QY 167 GACTCGAAGAAGGCGAGCAGCTCCGGTGCAGCAGCACCTTATCGTAGAAGGTGTCAACC 108
Db 162 rProAsnArgArgArgArgGluProTrpProProSerProTrpAlaSerArgAla---G1 181
QY 107 GCAGCTTCACTGCTTCTGCGCCCGCCAGGTGCATCAACAGCTTCTTGGCGCCGATCCC 48
Db 181 yProAlaSerCys-----GlyArgPro-----ProAlaCysSerProValAla 195
QY 47 GCTTCCGCTCTCTGCTGCTGTGCTGCGCGCTGTCAGGCGAGCG 2
Db 195 aThrAlaProThrAlaThrCysSerProProSerAlaArgSerAla 210

RESULT 5

US-09-252-991A-27249
; Sequence 27249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27249
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27249

Alignment Scores:
Pred. No.: 2,87e-05 Length: 308
Score: 130.50 Matches: 77
Percent Similarity: 36.59% Conservative: 13
Best Local Similarity: 31.30% Mismatches: 81
Query Match: 11.63% Indels: 75
DB: 4 Gaps: 17

US-09-920-953-2 (1-598) x US-09-252-991A-27249 (1-308)

QY 593 GGTGCGAAAAATGGCTGATGGCTTCAATGCAGCAGCGTGGCAACAGTTCAGGCT 534
Db 21 GlyAlaGlyProGlyArgGlyGlySer---GlyProGlyArgAlaGlyArgArgSerile 39
QY 533 CTGGGCGCCCTGGCGCGCTCGCAACTGCGCTCCCGCTCAAAATCGATGGAATGAG 474
Db 40 ProProAlaProArgArgGlyProArgLeuAlaArgProSerArgGlyArgGlyThr 59
QY 473 CGC-----TCAGGCTGGGTGGGT-----AATGAAATACAGTTG 438
Db 60 ArgAlaProGlyArgCysCysSerGlyTrp---TrpSerThrGlySer-ProMetAlaPr 78

QY 437 GGTGGCGAGTTGTTGGNAAGTCAAATTCGT-----CGCGGTGGACTCCACCACTCG 384
 Db 78 oValArgSerAlaCysArgGlyThrSerArgProValArgSerTrpProGlyProProAl 98
 QY 383 CGCGGTGTGTGATCAGTCTGCTTGTAGC-----CCATCTCTTGC 342
 Db 98 aglyArgAlaGlyGlyTyrglyArgArgGlyProArgArgSerValProProThrVa 118
 QY 341 AGCTGTCTCCAAAGTACTGCTTGATCT-----TGTCAAAGTGGCGGTGTC 294
 Db 118 lAlaSerValAlaGlyProSerArgSerGlyAlaGlyProAlaArgAlaAlaGlyPr 138
 QY 293 AGCGGTGGCCCTTGACCA----- 275
 Db 138 oGlyAlaAlaProCysProGlyProGlyArgGlySerGlyAlaAlaArgArgHisArgAr 158
 QY 274 -----GATGGCGTGTGCTGTACATGCTTCGCGCTTGTATGTTGCTGCTCG 225
 Db 158 gGlyArgArgProGlyArgArgSerArgTrpCys-----ProCysAlaGly---SerAr 175
 QY 224 CCAACACGAAGCTCATGACCTGACCTGCTTCATCTCTGCTTGTGATGTCAGGAC 165
 Db 175 gAlaArgArgProSer-----GlyCysThrGlyCy 185
 QY 164 TCGA-----AGAAGGCCA-----GCAGCTCGGCTCAGCCAGCACCTTA 126
 Db 185 sArgProArgLeuProArgArgAlaGlyArgArgAlaAlaGlyGlyArgProPro----- 203
 QY 125 TCGTAGAGGTCTCAACCCAGCTTCATGCTTCTGCGCCGCCAGGTCATCAA----- 71
 Db 204 -----CysCysProProGlyAla-----ProGlyGluArgLysAr 215
 QY 70 -----ACAGTTCTTCCGCGCGCATCCGCTTCGCGGCTCTGCTGCTGTCGCGCGG 15
 Db 215 gSerThrGluSerSerAlaArg---ProAlaPro-ArgProCysGlyGlySerGlyArgg 234
 QY 14 TCTGAGCGGCGGC 1
 Db 234 lAlaArgHisArg 238

RESULT 6

US-09-252-991A-29427
 ; Sequence 29427, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIORITY FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 29427
 ; LENGTH: 1476
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-29427

Alignment Scores:
 Pred. No.: 7,478-05 Length: 1476
 Score: 129.00 Matches: 74
 Percent Similarity: 38.01% Conservative: 10
 Best Local Similarity: 33.48% Mismatches: 91
 Query Match: 12.09% Indels: 46
 DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-29427 (1-1476)

QY 9 TGCAGACGCGGCCACCACCAACAGAGACGCGGAAGC-----GGGATGCGG 56

Db 492 CysArgArgAlaHisArgGlnHisArgGlnAlaAlaAlaAspAlaLeuGlyGlnArg 511
 QY 57 CGCAGAAGCTGTTTGTATGACCTGGCGCGCAGAGCATGAAGCTGGCGGTTTGACAC 116
 Db 512 ThrGlnLeuSerArg---ArgProGlyGlnLeuArgArgAlaProGlyHisArgAlaHis 530
 QY 117 CTTTACCATGAAGTGTGCTGCTGACCCGAGCTGCTGCTCTCTTCGAGTCCCTCGACAT 176
 Db 531 LeuProGlnLeuGlyAlaAla---ValGlyGlyAlaGlyLeuArgArg-----GlyHis 547
 QY 177 GCAAGACAGAGAAGATGAAGCAGGTCAAGTTCATGACTTCGTGTTGTCGAGCAGACCA 236
 Db 548 ArgProGlyArgTrpProValGlyLeuValArg-----ArgArgLeuPro 562
 QY 237 ATA-----CAAGGCGGAAGCATGTACGACGACACACCCCATCTGTCTAAGGGCACGG 290
 Db 563 AlaGlyArgArgGlyThrArgArgGlnGlyThrArgThrArgProGlyProGlyProAla 582
 QY 291 CTTGGA-----CCACCGCA-----CTTTGACAAGATCAACAGTA 326
 Db 583 ProGlyAlaGlyAlaAspArgProProAlaPheLeuLeuSerGlyAlaAlaArg 602
 QY 327 CTTTGGAGAGACGCTGCAAGAGATGGCGTCAA-----GCAGGATGTGATCCAGCACGC 380
 Db 603 Pro---ArgArgAlaGlyProAspArgGlnProProAlaGlyProAspProGlyArg 621
 QY 381 CGCGGAGTGTGAGTCCACCGC-----GACGAATTTGACTTNNCCCAACAA 428
 Db 622 ArgHisArgGlyAlaVal-ThrArgCysGlyAlaGlyThrGluAlaGlyValProArgPr 641
 QY 429 CTGCGCACCACTGATTTTCATTAACCAACCCACG----- 465
 Db 641 oProGlnProAlaAspGlyAlaThrAlaAlaAspGlnGlnGlyArgAspProGlySerHi 661
 QY 466 ---CCTGAGCGCTCATTCATTCGATTTTGGCGGGAGCGCGCATGTCGCGAGCGCGCCC 521
 Db 661 sProGlyArgAspAlaArgArg-----AlaThrValArgProArgPr 676
 QY 522 AGGGGGCCAGGAGCCTCAATCGTTTGCAGCGCTTGTGTCATTGAAGAGCCATCAG 580
 Db 676 cSerArgProAlaGly-GlnTyrHisProProAlaArgValAlaGlyLysArgHisArg 695

RESULT 7

US-09-252-991A-24046
 ; Sequence 24046, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24046
 ; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24046

Alignment Scores:
 Pred. No.: 7,81e-05 Length: 235
 Score: 126.00 Matches: 47
 Percent Similarity: 39.16% Conservative: 18
 Best Local Similarity: 28.31% Mismatches: 58
 Query Match: 11.23% Indels: 43
 DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-09-252-991A-24046 (1-235)

QY 482 TGAATGAGCGCTCAGC---TGG-----GGTGGGTTAATGAATCAG 441
 Db 26 TrpAspGlyArgSerGlyArgTrpSerArgTyrCysAlaTrp-----40
 QY 440 TTGGGTGCGCAGTGTGGGNAAGTCAAAATTCGTGCGGGTGAGCTCCACCACTCCGGCG 381
 Db 41 --GlyCysProSerValAlaProThrArgTrpSerArgGlyCysSerArgSerProPro 59
 QY 380 GCGTGTGGATACATCTCTGCTGAGCCCATCTTTGAGCGCTCTCTCAAGGTACTGC 321
 Db 60 CysAlaTrpAlaSerSerAlaIleThrProTrpProArgThrArgSerProSer-----77
 QY 320 TTGATCTTGCAAGTGGCGGTGCTGAGCGCGTGGCCCTTGACCATGGCGGTGCG 261
 Db 78 -----ArgArgTyrThrTrp---ArgSerTrp-----CysArgTrpGlyCysArg 91
 QY 260 TCGTACATGCTCGGCCCTTGATTGTCTGCTCCGCCCAACACAGCAAGCTCATGAATTC 201
 Db 92 -----ThrProProPro-Thr-----96
 QY 200 ACCTGCTTCACTTCTGCTCTTGCATGTCAGGAGCTCGAAGAGGCGCAGCTCCGG 141
 Db 97 -----AlaSerAlaSerIleSerAlaProAlaAlaCysSerIleHisAlaAlaProGl 114
 QY 140 TCAGCCAGCACCTTATCGTAGAGGTGT-----CAACCGCCAGCTTCATGCCT 93
 Db 114 yValSerAlaSerAlaSerAlaArgCysAlaCysCysSerSerProGlySerGlyGl 134
 QY 92 TCTGCGCGCCAGGTCAATCAACAGCTTCTTGCGCCCGCATCCGCTTCGCGCTCTCT 33
 Db 134 yCysArgArgProSerSerAlaCysSerSerThrAla---ThrProArgProThrGlyAr 153
 QY 32 GTGGTGTCTGGTGGCG 17
 Db 153 gTrpProArgTrpPro 158

RESULT 8
 US-09-252-991A-19344
 ; Sequence 19344, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 19344
 ; LENGTH: 394
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-19344

Alignment Scores:
 Pred. No.: 0.000107 Length: 394
 Score: 125.50 Matches: 68
 Percent Similarity: 31.82% Conservative: 16
 Best Local Similarity: 25.76% Mismatches: 76
 Query Match: 11.76% Indels: 104
 DB: 4 Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-19344 (1-394)

QY 17 CGGCCACGACGACACGACGAGCG-----CGG 43
 Db 116 ArgProGlyAlaProGluProArgGlyThrProProValGlyProGlySerLeuSerArg 135

QY 44 AAGCGGATCGCGGCGCAAGAAGCTGTTTGTATGACCTGGCGCG-----CCGAG 91
 Db 136 ArgLysProAlaGly-AspLeuAla-----ProProArgGlnLeuAlaAspArgPr 152
 QY 92 AAGCGATGAAGTGGCGGTGACACCTTCTACGATGAAGTGGCTGACCCCGAGGTGC 151
 Db 152 oAlaHisProProGlyGlySerHisLeuGlnLeuProGlyAlaGlyProProGlyArgVa 172
 QY 152 T-----GCCCTTCTTCGA-----164
 Db 172 largProAlaValSerLeuProProAlaValPheArgLeuHisGlnProAlaValAr 192
 QY 165 -----GTCCCTGGATCATCAAGACAGACAGAAGATGAAGCGTCAAGTTCATGAGTTCG 217
 Db 192 gArgProLeuProGlyHisAlaAla-----AlaGlyArgThrHisProGlnAl 209
 QY 218 TGT-----TGGCGGAGCAGACCAAT 238
 Db 209 aValProProAlaLeuSerArgArgProAlaGlyAlaProGlyArgArgGlnProAs 229
 QY 239 ACA-----GGCCCGAAGCATGTACGAGCAGCACACCCCATCTGTCAGGGCCACGGCTCG 295
 Db 229 pGlnProAspProProProAlaArgProArgLeuProAlaLeuAlaGlyProArgProGl 249
 QY 296 ACCACCGCCACTTTGAAGATCAAGCATCAAGCATCAAGTGGAGAGACGCTGCAAGAGATGGCG 355
 Db 249 yArgProProThrAlaHisGluPheAlaAspProAlaThrProProAlaArgGlyArgAr 269
 QY 356 TCAA-----359
 Db 269 gGlnLeuProAlaThrGlnGlyProProAlaAlaArgProGlyAspLeuProProGlySe 289
 QY 360 ---GCAGGATGTATCCAGCAGCAGCGCGGAGTGGTGAGTC-----398
 Db 289 rGlyArgAlaValAspProGlyHisArgArgAlaAlaArgLeuPheArgAlaLeuGlyLe 309
 QY 399 -----CACCGCGCAGAAATTTGACTTTCCTNCCCAACA 427
 Db 309 uProSerArgValGlnGluValAspArgProHisProArgArgVal-----324
 QY 428 ACTGCGCACCACTGATTTTCACTTAACCAACCCAGCCTGAGCGCTCATTCATCGAT 487
 Db 325 -----ProAlaProGlyGlySerLeuLysLeuSerPr 335
 QY 488 TTTGAGCGGAGCGCCAGTTCGCGAGCGCGCCAGGGCGCCAGGAGCCTGCAAAATCGT 547
 Db 335 oThrProGlyAspGluAlaArgCysAlaValAlaGlyArgAlaProTrpArgThrAlaAla 355
 QY 548 TTGCGAGCCC 557
 Db 355 aAlaArgPro 358

RESULT 9
 US-09-252-991A-19787
 ; Sequence 19787, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 19787
 ; LENGTH: 312
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-19787

Alignment Scores:
Pred. No.: 0.000142 Length: 312
Score: 124.00 Matches: 59
Percent Similarity: 37.70% Conservative: 13
Best Local Similarity: 30.89% Mismatches: 73
Query Match: 11.62% Indels: 46
DB: Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-19787 (1-312)

QY 9 TGCAGACGGCGCCACACAGACAGACGGCGGAGCGGATCGCGGCCACAGAGCT 68
DB 39 CysArgArgProGluGlnHisAlaProHisArgGlyAspGlyArgAlaTrpArg--- 57
QY 69 GTTGTAGACCTGGCGGCGGAGAGGACATGAGCTGGCGGTGACACCTTCTACGATAA 128
DB 58 -----GlyHisArgArgProSer----- 63
QY 129 GGTGCTGGCTGACCGGAGCTGCTGCCCTTCTTCGAGTCCCTCGACATGCAGAGACGAA 188
DB 64 GlyLeuProArgProGlyArg-----LeuArgAlaSerAlaHisArgAlaGly 80
QY 189 GATCAAGACGGTCAAGTTCATGAGCTTCGTGTTGGCGAGC-----AGCCANTA 239
DB 81 HisArgAlaGlyGlnArgHisAlaLeuProAlaTrpArgThrAlaArgIleArgProAla 100
QY 240 CAAGGCGGAGCATGTACGACGACACGCCCA-----TCT 275
DB 101 AlaGlyProValAlaAlaThrArgGlnAlaProArgArgAlaLeuHisAlaProGlyAla 120
QY 276 GGTCAAGGCGGCGGCTGACACCGCCACTTTGACAGATCAAGCAGTACTCTGGAGA 335
DB 121 GlyArgGlyArg-----AlaProValArgArgAspProAlaThrProGlyThr 137
QY 336 GACGCT-----GCAAGATGGCGCTCAAGCAGGATGTGATCCAGCAGC 380
DB 138 GlyThrAlaAlaLeuLeuHisAlaArgGlyHisLeuAla-----HisArg 153
QY 381 CGCGGAGTGTGGAGTCCACCGCGACGAAATTTGACTTNCACCAACTGGCCACCA 440
DB 154 ProGlyThrGlyProAlaAlaGlyAlaArgValLeuArgArgProArgLeuArgProGln 173
QY 441 CTGATTTC---ATTAAACCAACCCAGCTGAGCGCTCATTCATCGATTTTGACGGG 497
DB 174 ArgLeuHisArgLeuHisProAla-----GlyArgArgProArgSerAlaAlaGly 190
QY 498 GAGCGCAGTGGCGGAGC---GCGCCAGGGG 527
DB 191 ArgArgGlnGlyProAlaArgLeuProArgGly 201

RESULT 10
US-09-252-991A-20675

; Sequence 20675, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20675
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20675

Alignment Scores:
Pred. No.: 0.000318 Length: 726
Score: 122.00 Matches: 74
Percent Similarity: 32.13% Conservative: 6
Best Local Similarity: 29.72% Mismatches: 74
Query Match: 11.43% Indels: 95
DB: Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-20675 (1-726)

QY 2 CGCTGCTGCAGACG-----CGGCACACGACACACAGACGCGGAGCGGATGCG 55
DB 299 ArgAlaLeuArgThrGluArgHisProProAspProGlyArgHis-GlyProProAlaAr 318
QY 56 GCGCGAAGAGCTGTTGTATGATCGCTGGCGGCGAGAGG-----CATGAAGC 103
DB 318 g-----ProAlaAlaArgArgAlaAlaAlaValGlyGluAl 331
QY 104 TGGC-----GGTTGACACCTTCTACGATAAGTGCTGGC-----TGACCGGAGC 148
DB 331 aGlyAlaAlaGlyGlnGlyProArgArgThrGlyAlaAlaArgThrGlnSerProGlySe 351
QY 149 TGTGCGCTTCTTCGAGTCCCTGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTCA 208
DB 351 rAlaGlySerAlaAlaLeuArgAlaHisArgArgAlaGluGlySerAla-----AlaG 369
QY 209 TGAGCTTCGGTGT-----TCG----- 224
DB 369 yGluLeuArgAlaArgProGlyProTrpProAlaAlaGlnGlnProAlaSerAlaAlaPr 389
QY 225 -----CGGAGCAGACCAATACAAGG 244
DB 389 oAlaProGlyGluGlyArgGlyThrAlaArgAlaAlaArgArgGlnAlaAlaArgGlnAr 409
QY 245 GCGAAGCATGTACGACGACACGCCATCTGTCAGAGGCGCCAGCGCTGGACCCGCC 304
DB 409 gProThrAlaValArgThrAspArgGluAspGlnGlyArgProArgProProPr 429
QY 305 ACTTTGACAA-----GATCAA-----GCAGTACCTTGGAGCACCTGCAAG 346
DB 429 oProAlaGlnProGluAspGlnProAlaProAlaAlaAlaProGlyArgAspAlaAlaAr 449
QY 347 AGAT----- 350
DB 449 gAspAspProGlnArgThrHisGlyThrAlaProAlaGluGlyAlaAlaGlnProGlnAr 469
QY 351 -----GGCGCTCAAGCAGGAGTGTGATCCAGACGCGCGGAGTGTGAGT 397
DB 469 gGlnProAspHisGlyArgHisGlnProGlyAspProGlyValLeuProArgGlyGlyAl 489
QY 398 CCACCCGCGAGAAATTGACTTNCACCAACTCGGCACCACTGATTTTTCATTAACCC 457
DB 489 aArgProArg-----GlnProArgAlaArgGlyArgHisGlyGlnPr 503
QY 458 AACCCCGCTGAGCGCTCATTCATCGATTTTGAGCGGAGCGGAGTTCGCGAGCGC 517
DB 503 o-----HisGlyArgArgHisLeuProAl 512
QY 518 GCCCAGGGGCGCCAGAGCCTGCAA 542
DB 512 aGlnArgGlyGluProAlaLeuArg 520

RESULT 11
US-09-252-991A-17837

; Sequence 17837, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

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; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17837
; LENGTH: 204
; TYPE: PRN
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17837

```

Alignment Scores:	
Pred. No.:	0.000223
Score:	121.50
Percent Similarity:	34.56%
Best Local Similarity:	27.65%
Query Match:	11.39%
DB:	4
Length:	204
Matches:	60
Conservative:	15
Mismatches:	77
Indels:	15
Gaps:	14

US-09-920-953-2 (1-598) x US-09-252-991A-17837 (1-204)

Qy	5	TGCTGCAGACGCGGCCACCAAGCAGACCGCGGATGCGGGCGCAGA	64
Db	7	CysSerThrArgProProThrTrp-----ProSerAlaAen	21
Qy	65	AGCTGTTGATGACCTGGCGCGCAGAGGATGAAGCTGGCGTTGACACCTTCTACG	124
Db	22	SerMetAlaThrAlaIatrpProPheProAlaAlaSerTrpArgGthr-----Thr	39
Qy	125	ATAAGGTGCTGG-----CTGACCGCGAGCTGC-----	151
Db	40	SerArgCysCysAlaProAlaThrAspArgSerCysSerThrAlaThrSerGlyIleArg	59
Qy	152	TGCCCTTCTTCAGTCCCTGGACATCAAGACAGAGATGAAGCAGGTCAAGTTTCATGA	211
Db	60	CysGlyThrSerArgProTrp---AlaGlySerArgProProArgSerSer-----	76
Qy	212	GCTTCGTGTTGGCGGAGCAGACCAATCAAGGGCGCAAGCATGTACGACGACACACGCC	271
Db	77	-----ArgGluProGluProCys-----ArgAlaPro	85
Qy	272	ATCTGGTCAAGGGCCACGGCCTGGACCCACCGCCACTTTCACAAGATCAAGCAGTACTTG	331
Db	86	ProTrpSer-----AlaAlaIatrp-----AlaAlaThrCys	95
Qy	332	GAGACACGCTCAAGAGATGGCGTCAACGAGGATGTATCCAGACGCGCGCGGATGG	391
Db	96	ProArgProCysSerAlaThrThrCysSer-----ProProSerTrp	109
Qy	392	TGGAGTCCACCCGCGACGGAATTTGACTTNCCCAACACTCGCCACCCAACTGATTTTCAT	451
Db	110	ThrLeuProThrProGlySerAlaAlaAlaProAlaCysAlaSerGlyIle-----	126
Qy	452	TAAACCAACCCAGCCTGAGCGCTCATTCATCGATTTTCAGCGGGAGCGCCAGTT---	508
Db	127	-----SerProAlaThrSerAla---AlaAlaThrTrpProCysGlyArgProProPro	143
Qy	509	-----GCCGAGCGCGCCCGAGGGGCCAGGAGCCTGCAAAATCGT	547
Db	144	ArgSerProArgArgGlyTrpSerGluSerMetArgTrpCysTrpGlnProAla-----	161
Qy	548	TTGCCAGCCCTTGCTGCATTTGAAGGCCATCAGCCATTTTCGCACCAAGCC	598
Db	162	---ProAlaThrSerAlaIatrpProProArgProGlySerArgAla	177

RESULT 12

RESUM 12
US-09-252-991A-18476
; Sequence 18476, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND A

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

```

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196 136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18476
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-18476

```

Alignment Scores:	
Pred. No.:	0.000274
Score:	121.50
Percent Similarity:	33.50%
Best Local Similarity:	28.57%
Best Overall Similarity:	11.39%
Query Match:	4
DB:	
Length:	351
Matches:	58
Conservative:	50
Mismatches:	58
Indels:	77
Gaps:	10

115-09-920-953-2 (1-598) x US-09-252-991A-18476 (1-351)

Qy	30	CACAGACGCGCGGAACGGGATCGCGGCGCAAGAAGCTGTTTATGACCTGGGCGGCGC	89
Db	131	HisArgAlaAlaGlyArgGlyProAlaAlaGlyProSerGlyProArgProGlyArgArg	150
Qy	90	AGA-----AGCATCAAGCTGGCGTTGACACCTTCTACGATAAGGT	131
Db	151	LysProAlaValArgProAlaArgHisAlaAlaProAla-----	163
Qy	132	GCTGGCTCACCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGA-----CATGCA	179
Db	164	-----ProGlyLysAspProArgArgArgArgGlyAspGlnGluProHisArg	180
Qy	180	AGACGAGAAGTAAAGCAGGTCAAGTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATA	239
Db	181	AlaAlaArgArgAlaGlyGlyAlaHis-----ArgProTrpArg---ArgProLeu	197
Qy	240	CAAGGCGGAGCATGTACGACGACACGCCCATCTGTCAAGGCCACGGCCTGGACCA	299
Db	198	ProGlyProAspHisProArgGlyGlyGlnProAlaGlyGlyLeProHisAla-----	215
Qy	300	CGGCCACTTTGACAAGATCAAGCAGTACCTTGGAGAGACGCTGCGAAGAGATGGGGCTGAA	359
Db	216	-----AlaIleArgArgGlyArgGln-----	222
Qy	360	-----GCAGGTGTGATCCACGA-----CGCCGCGCGG	386
Db	223	AlaLeuArgAlaGlyArgGlnProAlaProAspArgProLeuHisArgArgArgArg	242
Qy	387	AGTGTGGAGTCCACCCCGCAGCAATTTGACTTNCACCAACATCGCGCACCCCACTGATT	446
Db	243	ProGlyAlaValAlaProAlaArgLeuGlyAsnLeuAlaGluGlyGlnAlaGln-----	260
Qy	447	TTCATTAAACCAACCCCAAGCCTGACCGCTCATTCATCGATTTTGAGCGGGGAGCGCCAG	506
Db	261	-----GlyArgArgAla-----	264
Qy	507	TTGCG-----AGCGCGCCCGGGGGCCAGGAGC	536
Db	265	GlyProArgArgArgArgAlaAlaArgHisLeuArgProProArgArgProArgArg	284
Qy	537	CTGCAAAATC	545
Db	285	LeuArgVal	287

RESULT 13

US-09-252-991A-20161
; Sequence 20161, Application US/09252991A
; Patent No. 6551795

```

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20161
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20161

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Alignment Scores:
Pred. No.: 0.000271 Length: 248
Score: 121.00 Matches: 47
Percent Similarity: 35.11% Conservative: 19
Best Local Similarity: 25.00% Mismatches: 62
Query Match: 11.34% Indels: 60
DB: 4 Gaps: 11

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US-09-920-953-2 (1-598) x US-09-252-991A-20161 (1-248)
QY 2 CGCTCCCTGACGCGGCCACACCA---CCACAGACGCGCGGAAGCGGATCGGCGC 58
Db 56 ArgCysAlaArgSerProProAlaGlyProSerThrThrArgArgProAlaSer 75
QY 59 GCAAGA---AGCTGTTGATGACCTGGCGCGCAGAGGCGATGAGTGGCGTTGACA 115
Db 76 AlaSerIleArgCys-----SerAlaArgValArgLysTrpTrpSerThr 90
QY 116 CCTTCTACATGAAG-----130
Db 91 SerAlaThrIleArgLysAsnSerAlaAlaAsnThrLysAlaAlaArgTrpCysArg 110
QY 131 -----TGCTGCTGACCGGAGC-----TGCTGC-----154
Db 111 ArgCysAlaCysTrp---ThrArgAsnArgProAlaArgSerCysArgCysValAla 129
QY 155 -----CCTTCTGAGTCCCTGGACATGC 178
Db 130 ThrArgSerSerAlaProProThrThrProProAlaProThrSerIleProThrProCys 149
QY 179 AAGAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTTTGGCGGAGCAGACCAAT 238
Db 150 ThrArg-----AlaThrCysAlaAlaSerAlaAla---159
QY 239 ACAAGGCGGAGAGCATGTACGACGACGCGCCATCTGTCGAAGGCGCACGCGCTGGACC 298
Db 160 ThrArgGlyArgSerCysAlaThr---ThrLysArgTrpArgSerAlaGlySerThrAla 178
QY 299 ACCGCCACTTTCACAGATCAAGCATGACCTGGAGAGACGCTGCAAGAGATGGCGCTCA 358
Db 179 ProGlyLysSerAlaAlaThrProAlaThrThrAlaArgArgCys-----TrpSerThr 196
QY 359 AGCAGGATGTGATCCAGCAGCGCGCGGAGTGGTGTCCACCGCGCAGCAATTTGACT 418
Db 197 ProGlnAlaProGlyAlaThrProSerProGlyTrpProAlaSerAlaArgTrpAlaCys 216
QY 419 TNCACCAACTGGCGACCAACT 442
Db 217 SerProSerAlaAlaGlnProSer 224

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RESULT 14
US-09-252-991A-20509
; Sequence 20509, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

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; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20509
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20509

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Alignment Scores:
Pred. No.: 0.000398 Length: 686
Score: 121.00 Matches: 51
Percent Similarity: 35.22% Conservative: 5
Best Local Similarity: 32.08% Mismatches: 47
Query Match: 11.34% Indels: 56
DB: 4 Gaps: 9

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US-09-920-953-2 (1-598) x US-09-252-991A-20509 (1-686)
QY 3 GCTGCTGACAGCGGCGCCACGACCAACAGAGCGGGAAGCGGATCGGCGGCA 62
Db 117 AlaAlaCysArgArgGlyAlaTrpHis-----GlyLeuArgProArg 130
QY 63 GAAGCTGTTTCATGACCTGCGCGCGCGAGAGGATGAAGTGGCGGTTGACACCTTCTA 122
Db 131 ProAla-----GlyArgArgArgProAlaAlaGlyGly-----142
QY 123 CGATAAGGTGCTGGTGTGACCGCGAGCTGCTCCCTTTCGAGTCCCTGGACATCAAGA 182
Db 143 -----GlnArgTyrAlaAlaGluArgCysAlaGlyLeuAlaArg 155
QY 193 CGAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTTGG-----224
Db 156 ProAlaProArgThr-----ValAlaArgArgArgProTrpArgHisProArgCysAla 173
QY 225 -----CGAGCAGACCAATACAGGCGCGAGCATGTACGACGACACACGCGCCATCTGCT 278
Db 174 ValProArgGlyArgProAlaAlaGlyAla-----AlaAlaArgArgArgGlyAlaGly 191
QY 279 CAAGGCGCACGCGCTGGACACCGCCACTTTTGACAAGATCAAGCATGACCTTGGAGAGAC 338
Db 192 GlyGlyIleGlnProGlyLeuPro-----CysLeuAlaTrpArgAla 205
QY 339 GCTGCAAGA-----GATGGCGGTCAA 359
Db 206 AlaAlaArgGlyLeuAlaArgLeuProProGlyGlnProTrpAlaThrGlyAlaArgGln 225
QY 360 GCAGGATGTGATCCAGCAGCGCGCGGAGTGGTGA-----GTCCACCCG 404
Db 226 ProGlyAlaGlyAlaGlyProArgArgGlyGlyGlyValArgArgThrHisPro 244

```

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RESULT 15
US-09-252-991A-23215
; Sequence 23215, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

```

; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 23215
 ; LENGTH: 219
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-23215

Alignment Scores: Pred. No.: 0.000331 Length: 219
 Score: 120.00 Matches: 57
 Percent Similarity: 38.27% Conservative: 18
 Best Local Similarity: 29.08% Mismatches: 72
 Query Match: 10.70% Indels: 49
 DB: 4 Gaps: 9

US-09-920-953-2 (1-598) x US-09-252-991A-23215 (1-219)

QY	593	GGTGCAGAAATGGCTGATGGCTCTTCAATGCAGAGGGCTGGCAACGATTTCAGGCT	534
DB	58	GlyArgArgTyrSerAspArgSerAlaPro-----AlaAsnProProGly	73
QY	533	CCTGGCCCCCTGGCGCGCTCGCAACTGGCGCTCCCC-----GCTCAAAATCGA	483
DB	74	ProGlySerValProArgSerArgTyrAlaValProGlyAlaAlaArgSerArg	93
QY	482	TGGAATGAGCGCTCAG-----GCTGGGTTGGTTAATGAAATCAGTTGGGT	435
DB	94	-ProAlaThrGlyProProArgTrpAlaGlyProGlyHisArgAlaAlaAlaTrpLe	113
QY	434	CGCAGTGTGGGNAAGTCAAAATTCGTCGGCGGTGGACTCCACCACCTCCGCGCGGTGC	375
DB	113	uArg-----ArgArgAlaSe	118
QY	374	TGGATCACATCTCTGTCAGCCCATCTCTTGAGCGCTCTCTCAAGGTACTGCTTGAIC	315
DB	118	rAlaSerCysProGlyHisArgArgGlyAspSerGlySerSerProGlyProArgLysAl	138
QY	314	TTGTCAAAGTGGCGGT-----GGTCCAGCGCTGGCCCTTGACCATGGCGGTGT	264
DB	138	aThrArgGlyHisGlyArgLysArgProProGlyArg-----ProAspAlaProVa	155
QY	263	CGCTCGTACATGCTCGCCCTTGTATTGCTCTGCTCCGCCAAACACGAAGCTCATCAAC	204
DB	155	lArgArg-----AlaProAlaAsnSerVal-----	163
QY	203	TTGACCTGCTTCATCTTCTGCTCTTGCAATCCAGGAGCTCGAAGAAGGCGAGCAGCTCC	144
DB	164	-----ProAlaSerArgGlyArgAlaGlyCysSerArgPheArgCysArgThrProAlaPr	182
QY	143	GGGTACGCCAGCACCTTATCGTAGAGGTGTCAACCGCAGCTTCATGCCCTTCTGCGCG	84
DB	182	oGlyAlaProAlaArgProAlaGlyArgSerProProAlaArgCys-----Ar	199
QY	83	CCGAGGTCAACAAACAGCTTCTTGGCGCGCTCCGCTTCGCGCG	38
DB	199	gSerGlyCysAlaAlaAlaArgGlyProProValProValProPro	214

Search completed: February 22, 2005, 21:22:43
 Job time : 37 secs

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 58160
LENGTH: 324
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73219F07_FLI.pep
US-10-425-114-58160

PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 61519
LENGTH: 124
TYPE: PRT
ORGANISM: Legionella pneumophila
US-10-282-122A-61519

Alignment Scores: 124
Pred. No.: 7,12e-16
Score: 254.50
Percent Similarity: 64.10%
Best Local Similarity: 41.88%
Mismatches: 41
Indels: 1
Query Match: 23.85%
Gaps: 15
DB:

US-09-920-953-2 (1-598) x US-10-282-122A-61519 (1-124)

Qy 61 AAGAAGCTGTTGATGACCTGGCGCGGAGGATGAGTGGCGGTTGACACCTTC 120
Db 3 GluSerLeuPheGluArgLeuGlyGlnAsnAlaValAsnThrAlaValAspIlePhe 22
Qy 121 TAGATTAAGTGTGGCTGACCCGAGCTGCTGCCCTTCTTCAGTCCCTGGACATGCAA 180
Db 23 TyrArgLysMetLeuMetAspArgValAsnTyrPhePheAspValAspMetGlu 42
Qy 181 GACGAGAGATGAAGCAGGTCAAGTTCATGAGCTTCGTGTTGGCGGAGCAGACCAATAC 240
Db 43 GlnGlnIleLeuLysGlnLysGlyPheLeuThrMetValPheGlyGlyProAsnGlnTyr 62
Qy 241 AAGGCGGAGAGTACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 300
Db 63 ThrGlyLysSerMetArgGluGlyHisGlnHisLeuLeu---AlaArgGlyLeuAsnAsp 81
Qy 301 CGCCACTTTCACAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAG 360
Db 82 SerHisValAspIleValIleGluHisLeuGlyGluThrLeuLysGluLeuGlyAlaAsn 101
Qy 361 CAGGATGTGATCCAGCAGCGCGCGGAGTGGTGGAGTCCACCCGCGAGAA 411
Db 102 GluGluAspIleGlnLysValAlaAlaIleAlaAsnSerValArgGlyAsp 118

RESULT 2

US-10-425-114-58160
Sequence 58160, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei

Alignment Scores: 324
Pred. No.: 2.08e-05
Score: 148.00
Percent Similarity: 38.10%
Best Local Similarity: 19.52%
Query Match: 13.87%
Indels: 53
Gaps: 10
DB:

US-09-920-953-2 (1-598) x US-10-425-114-58160 (1-324)

Qy 5 TGCTGTGACAGCGCGG-----CCACAGACACACAGAGAGCGGCGGAAGCGG 49
Db 84 CysAlaArgThrArgAlaArgThrAlaProSerAlaProCysThrArgArgThr 103
Qy 50 GATCGGCGGCGAAGAGCTGTTGATGACCTGGCGGCGGAGAGCATGAGCTGGCGG 109
Db 104 SerSerGlySerArgAlaCys-----110
Qy 110 TTGACACCTTCTACGATAAGGTGCTGG-----CTGACCGGAGCTGCTGC 154
Db 111 -----ProSerAlaAlaThrCysTyrArgTyrAlaAlaThrArgSerArgProThrSer 128
Qy 155 CCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAGATGAGCAGGTCAAGTTCATGAGCT 214
Db 129 ProArgTyrGlyProTyrCysProSerProSer---SerCysSerSerSerAla 147
Qy 215 TCGTGTTTGGCGGAGCAGCAATACAAAGGCGGCGGAGCATGACGACGACGCGCCATC 274
Db 148 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProgl 167
Qy 275 TGCT-----CAAGGCGGCGGCTGGACCAACCGCCACTTTGACAGATCAAGCAGTACC 328
Db 167 nGlyThrProArgProProArgPro--ThrSerArgThrSerSerAlaArgSerThr 186
Qy 329 TTGAGAGACCTGCAAGAGA-----TGGGCGTCAAGCAGGATGTGATCC 373
Db 187 -----SerAlaCysThrArgProAlaAlaThrCysTyrSerThrCysArgAlaThrTrp 204
Qy 374 AGCAGCGCGCGGAGTGGTGGAGTCCACCCGCGACGAATTTGACTTCCCAACACTGCG 433
Db 205 AlaCysAlaThrProThrTyrArgProProAlaProArgCysThrAlaSerAlaThr--- 223
Qy 434 CACCAACTGATTTTCATTAAACCCCAACCCGAGCTGAGCGCTCATTCATCGATTTGAG 493
Db 224 -----ProGlnAlaAlaAlaSerGlyThrSerTyrArg 234
Qy 494 -----CGGGAGCGCGAGTTCGCGGCGCGCGCGGCGCGCGCGCGCGCGCGCGCG 541
Db 235 ThrTrpArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 253
Qy 542 AATCGTTTGGCGGCGCGCTTGTGCA 565
Db 254 GlyArgAlaSerSerAlaThrAla 261

RESULT 3

US-10-084-846A-5
Sequence 5, Application US/10084846A
Publication No. US20040006026A1
GENERAL INFORMATION:

; APPLICANT: WEITNAUER, GABRIELE
 ; APPLICANT: MUHLENWEG, AGNES
 ; APPLICANT: TREPZER, AXEL
 ; APPLICANT: BECHTHOLD, ANDREAS
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 ; FILE REFERENCE: 1974-005
 ; CURRENT FILING DATE: 2003-02-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4
 ; PRIOR FILING DATE: 2001-02-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 5
 ; LENGTH: 19723
 ; TYPE: PRT
 ; ORGANISM: Streptomyces viridochromogenes
 ; FEATURE:
 ; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
 ; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
 ; US-10-084-846A-5

Alignment Scores:
 Pred. No.: 0.000206 Length: 19723
 Score: 142.50 Matches: 63
 Percent Similarity: 34.96% Conservative: 16
 Best Local Similarity: 27.88% Mismatches: 68
 Query Match: 13.36% Indels: 79
 DB: 15 Gaps: 12

US-09-920-953-2 (1-598) x US-10-084-846A-5 (1-19723)

QY	5	TGCTGACAGCGCGCCACAGACAGACAGCGGGAGCGGGATGCGGGCGCAAGA	64
Db	4635	CysAlaAlaArgSerProSerPro-----AlaTrpSerThr	4647
QY	65	AGCTGTTGATGACCTGG-----GCGGCGCAGAAGCATGAAGCTGGCGGTG	112
Db	4648	SerAlaProAlaThrTrpSerTrpThrSerAlaAlaThrAlaProCysTrpArgPro	4667
QY	113	ACACCTTCTACGATAAGTCTGGCTG-----TTGGCGGAGCAGACC	235
Db	4668	ThrProThrGlyProAlaTrpSerGluTrpThrProProProSerSerProArg	4687
QY	140	-----ACCGG-----AGCTGCTGCTTCTGAGTCCCTGGACATGCAAGCAGCAAGA	190
Db	4688	ProThrArgArgAlaSerSerProThrSerSerHisThrThrCysSerAlaGlyAla	4707
QY	191	TGAAGCAGGTCAAGTTCATGAGCTTCGTG-----TTGGCGGAGCAGACC	235
Db	4708	AlaProArgSerSerProArgSerArgCysSerThrThrCysArgValProTrpSerSer	4727
QY	236	AATACAAGGCGCGAAGCATGTACGACG-----TTGGCGGAGCAGACC	262
Db	4728	CysGlyArgSerAlaAlaCysArgThrThrAlaSerGlyProSerArgAlaIleCysPro	4747
QY	263	-----CACACGCCC-----ATCTGTCAGGCGCCAGCGCTGGACACCGCCACT	307
Db	4748	ArgCysSerThrProAlaProThrThrTrpSerAlaThrSerThrTrpThrThrGly	4767
QY	308	TTGCACAGATCAGCAGTACTCTGGAGAGCGCTGCAAGAGATGGCGTCAAGCAGGATG	367
Db	4768	CysAlaArgSerGly-----TrpProSerAla-----	4777
QY	368	TGATCCAGCAGCGCGCGAGTGGTGG-----AGTCCACCGCGAGAAATTTGACTTNC	421
Db	4778	-----ProAlaArgTrpTrpMetProSerProProSerThr--AlaGluAla	4793
QY	422	CCAACAACCTGGCACCACCACTGATTTTCATTAAACCCAA-----	459
Db	4793	erArgSerCysTrpProAlaAlaAlaProLeuAlaArgSerThrSerArgArgTrpProA	4813

QY	460	-----CCCCAGCCTGAGCGCTCAATTCATCGATTTTGAGCGGGAGCGCAGTTCGCCGAGCG	517
Db	4813	laSerAlaProGluArgArg-----ThrCysProThrArgSerS	4826
QY	518	GCCACAGGGGGCCCA	531
Db	4826	erProGlyGlyPro	4830

RESULT 4

US-10-437-963-143835
 ; Sequence 143835, Application US/10437963
 ; Publication NO. US2004012343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 143835
 ; LENGTH: 417
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_44705C.1.pap
 ; US-10-437-963-143835

Alignment Scores:
 Pred. No.: 0.00384 Length: 417
 Score: 125.00 Matches: 63
 Percent Similarity: 36.19% Conservative: 13
 Best Local Similarity: 30.00% Mismatches: 74
 Query Match: 11.72% Indels: 60
 DB: 16 Gaps: 10

US-09-920-953-2 (1-598) x US-10-437-963-143835 (1-417)

QY	23	CCAGCACCACAGACGCGGAGCGGGATGCGGGCGCAAGAGCTGTTGTGATGACCTGG	82
Db	22	ProThrProHisArgArgGlu-----IleGluArgTrp	32
QY	83	GCGGCGCAGAAGCATGAAGCTGGCGGTTGACACCTTCTACGATAGGTGCTGGCTGACC	142
Db	33	Leu-----ProTrpArgSerAlaProPro-----ThrThr	43
QY	143	CGGAGCTGCTGC-----CCTTCTCGAGTCCCTGGACATGCAAGACGAGA	187
Db	44	GlySerCysSerThrProThrProProProProThrThrThrSer---	62
QY	188	AGATGAAGCAGGTCAAGTTCATGAGCTTCGTGCGGAGCAGACCAATACAAAGGCC	247
Db	63	-----SerArgSerLeuProAlaThrProProProAlaProThrLysArgArg---	79
QY	248	GAAGCATGTACGACGACACGCCCATCTGCTCAAGGCGCCACGGCCTGGACACCGCCACT	307
Db	80	-----ArgThrThrArgTrp---GlyAlaThr	87
QY	308	TTGACAAGATCAAGCAGTACCTTGGAG-----AGACGCTGCAAG	346
Db	88	LeuThrAlaThrSerThrAlaGluAsnSerArgArgArgThrArgArgAlaArgArg	107
QY	347	AGATGGCGCTCAGCAGGATGTCTCAGCAGCCCGCGAGTGGTGGAGTCCA-----	400
Db	108	ArgArgGlyArgSerArgAlaSerSerThrThrProProProThrThrSerProGlyThr	127

Fri Feb 25 16:26:58 2005

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QY 401 ---CCCGGACGAAATTTGACTTNNCCCAACAACTCGGCACCCCACTGATTTTCATTACCC 457
Db 128 SerProSerThrProSerAlaAlaProSerThrSerProAlaSerProPro 147
QY 458 AACCCACCGCTGAGCGCTCATTCATCGATTTTGGCGGGGAGCGCCAGTGGCGAGCGC 517
Db 148 TyrArgSerThrProSerProPro--ProAlaAlaSerSerAlaSerAlaAla 167
QY 518 GCCACGGGGGCCCA-----GGAGCCCTGCAAAATCGTTTG 550
Db 167 TgProProAlaProThrThrSerProThrArgProProSerGlyCysAlaSerLeuA 187
QY 551 CCAGCCCTTGTCATTTGAAGAGCCA 576
Db 187 laThrProAlaThrThrSerThrPro 195

RESULT 5
US-10-084-846A-3
; Sequence 3, Application US/10084846A
; Publication NO. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 19695
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-3

Alignment Scores:
Pred. No.: 0.0104 Length: 19695
Score: 125.00 Matches: 57
Percent Similarity: 35.29% Conservative: 15
Best Local Similarity: 27.94% Mismatches: 68
Query Match: 11.72% Indels: 64
DB: 15 Gaps: 11

US-09-920-953-2 (1-598) x US-10-084-846A-3 (1-19695)
QY 2 CGTGGCTGCAGACG---CGGCCACAGACACACAGCGCGGAGCGGATGCGGCG 58
Db 11324 ArgCysAlaGlyThrSerAlaSerProAlaSerThrArgArgSerArgSerProAla 11343
QY 59 GCAGA-----AGCTGTTTGATGACCTGGCGCGCGAGGAGCGATGAAGC 103
Db 11344 AlaArgThrTrpArgCysGlyAlaAlaSerThrThrTrpAlaAlaGlyArgArg----- 11361
QY 104 TGGCGGTTGACACCTTCTACATAAGG-----TGCTGG----- 136
Db 11362 -----SerAlaAlaArgLysAsnCysTrpSerSerSerThrProArgPro 11376
QY 137 -----CTGACCGGAGCTGCTCCCTTCTTCGAGTCCCTCGACATGC 178
Db 11377 ProThrSerGlySerSerThrThrArgAlaValCysGlyAlaGlySerThrTrpProPro 11396
QY 179 AAGAGCAGAGATGAAGCAGTCA-----TGAGCTTCTGTTTG 223
Db 11397 AspSerProCysProArgCysSerSerThrTrpThrSerProProAlaSerThrArg 11416

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QY 224 GCGGACGAGCC-----AATACAAGGCCGGAAGCATGT 256
Db 11417 AlaThrAlaThrArgSerGlyArgTrpSerValArgTrpSerSerArgAlaProProCys 11436
QY 257 ACAGCCGACACGCGCCATCTGGTCAAGGCCACCGGCTCGACCGCCACTTTGACAAAGA 316
Db 11437 CysSerProArgSerThrTrpArg-----ProThrGlySerProThrArg 11452
QY 317 TCAAGCAGTACCTTGGAGAGACGCTCCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGC 376
Db 11453 SerArgSerThr-----ArgAlaAlaGlySerSerArgAlaProPro 11466
QY 377 ACGCCCGCGAGTGGTGGAGT-----CCACCCCGCGAGC--- 409
Db 11467 ArgProSerProTrpAlaAlaThrGlySerTrpProTrpArgProArgThrCys 11486
QY 410 -----AATTGACTTNNCCCAACAACTCGGCACCCCACTGATTTTCATTACCCCAAC 460
Db 11487 ArgProProArgLeuArgSerProAlaSerArgGlyProSerProArgTrpThrProArg 11506
QY 461 CCCAGCCTGAGC 472
Db 11507 ProAlaValSer 11510

RESULT 6
US-10-084-846A-6
; Sequence 6, Application US/10084846A
; Publication NO. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 19662
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 2.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-6

Alignment Scores:
Pred. No.: 0.0116 Length: 19662
Score: 124.50 Matches: 56
Percent Similarity: 33.02% Conservative: 14
Best Local Similarity: 26.42% Mismatches: 64
Query Match: 11.10% Indels: 78
DB: 15 Gaps: 10

US-09-920-953-2 (1-598) x US-10-084-846A-6 (1-19662)
QY 536 GTCCTCGGCGCCCTGGCGCGCTGGCAACTGGCG-----CTCCCGCTCAAAATCGATGG 480
Db 19332 AlaProGlyArgProProArgProArgProCysAlaGlyPheProThr----- 19347
QY 479 AATGAGCGCTCAGGCTGGGTTGGTTAATGAATCAGTTGGGTGGCGCAGTTGTTGGN 420
Db 19348 -----ProGlyProGlyTrp----- 19352
QY 419 AAGTCAAAATTCGTCGGGTGGACTCCACCACCTCGCGGGCGTGTGATCATCATCC--- 363

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Db 19353 -----AlaAlaAlaCysSerAlaAlaProCysSerCysSerAlaThrSerThr 19368
QY 362 -----TGCTTACGCGCCATCTCTTGCAGCGTCTCTCCA 330
Db 19369 ArgCysCysSerGlyArgArgSerArgCysThrAlaCysCysSerCysProCysAlaSer 19388
QY 329 AGGTACTGC---TTGATCTTGTCAAAGTGCGCG---TGCTCCAGG----- 291
Db 19389 ArgArgCysGlyCysAlaGlyAlaThrTyrArgProArgArgTyrTyrArgSerPro 19408
QY 290 ---CCGTGGCCCTTGACCATGGCGTGGCGTGCATGCTTGGCCCTTGTATTGG 234
Db 19409 SerProTyrGlyTyrCysArgTyrProThrAlaAlaGlyGlySerAlaAspThrTyrGly 19428
QY 233 TCTGCTCCGCCAACACG----- 216
Db 19429 SerSerProSerProProArgProGlyGlyCysThrGluGlyArgSerProValSer 19448
QY 215 -----AAGCTCATGAACCTTGACCTGCTTTCATCTTCTGCTCTTGCATGTCCAGG 168
Db 19449 SerProHisGlyArg-SerGlyCysTyrProAlaGlyProArgProAlaAlaGlyProG 19468
QY 167 GACTCGAAGAGGCGACAGCTCGGCGTCCAGCGACCTTATCGTGAAGAGTGTCAACC 108
Db 19468 YAspArgGlnAlaLeuSerSerGlySerPro----- 19479
QY 107 GCCAGCTTCATGCTCTTGGCGCGCCAGGTGCATCAACAGCTTCTTGGCGCCGCATCCC 48
Db 19480 -----ArgArgArgGlyAlaProSerPheSerAlaAlaArgIleAl 19493
QY 47 GCTTCCG-----CCGTCTCTGTGGTCTGTGGTG 20
Db 19493 aaAlaProThrIleProAlaLeuPheCysSerTyr 19504

```

RESULT 7

```

US-10-084-846A-8
; Sequence 8, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084, 846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 8
; LENGTH: 19608
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-8

```

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Alignment Scores:
Pred. No.: 0.0284 Length: 19608
Score: 120.50 Matches: 49
Percent Similarity: 35.71% Conservative: 16
Best Local Similarity: 26.92% Mismatches: 92
Query Match: 11.29% Indels: 25
DB: 15 Gaps: 7

```

US-09-920-953-2 (1-598) x US-10-084-846A-8 (1-19608)

QY 20 CCACGAGCACACAGAGCGCGAAGCGGGATCGGGCGCGAAGAAGCTGTTTGTATGACC 79

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Db 5430 ProProAla-----SerSerThrArgCysCys----- 5438
QY 80 TGGCGCGCGCAGAGCATGAAGCTGGCGTTTGACACCTTCTACGATAAAGGTCTGCGCTG 139
Db 5439 -----ProProAlaSerThrTyrArg-----SerThrAlaAlaCysTyrPro 5452
QY 140 ACCCGAGCTGTCGCCCTTCTTCGATCCCTGCAGATGCAAGAGCAGAGATGAAGCAGG 199
Db 5453 ArgArgProCysSerProArgThrArg-----ThrSerArgArgArgProGlyArg 5470
QY 200 TCAGTTTCATGACTTCGTGTTTG-----GCGGAGCAGACCAATACAAAGGCCGGAAGCATGT 256
Db 5471 SerThrSerArgSerThrAlaThrProThrSerGlyCysSerProTyrCysProAlaCys 5490
QY 257 AGCAGCCACACGCGCATCTGCTCAAGGCGCAGCTGGACACCGCCCTTTGACAAGA 316
Db 5491 ThrSerAsnArgProAlaArgProProThrSerSerTyrProThrArgProArgSerAla 5510
QY 317 TCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGAGATGTGATCCAGC 376
Db 5511 ProArgProSerThrSerArgSerThrAlaAlaArgTyrProSerProAsnTyrSerArgAsp 5530
QY 377 ACCCGCGGAGTGGTGGAGTCCACCGCGCAGCAATTTGACTTCCCAACA-----ACT 430
Db 5531 TtrProThrSerThrThrProSerProAlaAlaArgThrArgThrAlaProSerArgArgThr 5550
QY 431 GCGCACCAACTGATTTTTCATTAAACCCAGCTGAGCGCTCATTCATCGATTTT 490
Db 5551 ProArgProThrProCysArgArgThrThrProSerAlaSerCysSerArg----- 5567
QY 491 GAGCGGGGAGCGCGAGTTCGCGAGCGCGCCAGGGGGCCCGAGAGCTGCAAAATCGTTTG 550
Db 5568 ArgProArgThrProValTyrArgArgProGlyCysProHisArgSerAlaAlaArgLeu 5587
QY 551 CCAGCC 556
Db 5588 ProAla 5589

```

RESULT 8

```

US-10-437-963-166380
; Sequence 166380, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 166380
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(276)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_65095C.1.pap
US-10-437-963-166380

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Alignment Scores:
Pred. No.: 0.0118 Length: 276
Score: 119.50 Matches: 52

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us-09-920-953-2.rapb

Pred. No.:	0.0201	Length:	384
Score:	117.50	Matches:	69
Percent Similarity:	37.95%	Conservative:	16
Best Local Similarity:	30.80%	Mismatches:	74
Query Match:	11.01%	Indels:	65
DB:	15	Gaps:	13

29	CCACAGAGAGCGCGGAAGCGGGATCGGGCGCAAGAAGCTGTTTGATGACTCTGGCGGGCG	Qy
3	ProArgArgArgArgArgfileCysThrValArg	Db
89	CAGAAGGCATGAAGCTGGCGGTGACACCTTCTACGATAAGGTGCTGGCTGACCCGAGC	Qy
15	-----ArgProThrAlaThrThrThr-----ThrThrThrSer	Db
149	TGCTGCTCTTTCGAGTCCCTGGACATGCAAGAGCAGAGAAGATGAAGCAGGTCAAGTTCA	Qy
26	AlaSerProSerSerSerProThrPro-----GlySerSerProGly	Db
209	TGAGTCTCGTGTGTGGCGGAGCAGACCAATACAAGGGCGGAAGCATGTACGAGC-----	Qy
40	AlaAlaSerCysAlaThrSerSerAlaAlaSerArgAlaThrArgThrSerThrAlaPro	Db
263	---CACACGCCCATCTGTGTCGAAGGCCACGCGCTTGGACCCCGCCACTTTTGACAAGATCA	Qy
60	ProSerSerProSerHisGlySerArgSerProThrThrGlyThrThrSerSerProSer	Db
320	AGCAGTACCTTGGAGAGCAGCTGC-----AAGAGATGGCGCTCAACGACGATGTGA	Qy
80	ArgSerGlySerCysArgGlyCysCyspheArgArgArgTrpArgSerThrArg-----	Db
371	TCCAGCACGCCCGCGAGTGTGGAGTCCACCCGCGAGCAATTTGACTTNCACCAACT	Qy
98	-----ProProAlaProSerSerAlaSerProThrGly	Db
431	GGCACCACCACTGATTTTCATTAAACCCAGCCGCTGAGCGCTCATTCATCGATT	Qy
109	AlaSerThrThrSer-----ProSerProThr-----	Db
491	GAGCGGGAGCGCGTAGTTGCCGAGCGCCCGAGGGGCCAGGAGCGCTGCAAAATCGTTTG	Qy
118	-----ProAlaAlaArgAlaAlaSerGlyAlaProAlaAspGlySer***Cys	Db
551	CCAGCCCTTGCTGCATTGAAGAGCCATCAGCCA	Qy
134	SerGlyValAlaProArgGlySerSerAlaPro	Db

```

US-10-425-114-72136
; Sequence 72136, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72136
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-558-A1_FLI pep
US-10-425-114-72136

Alignment Scores:

```

CURRENT FILING DATE: 2003-04-28

385	QY	CGCGCGCGTGTGGATCACAATCCCTGCTTGACGCCCATCTCTTTCAGCGCTCTCTCCAAGT	326
19	Db	ArgArgAlaProThrHisGluPro-----ProSerSerProArgAlaGlyVargSer	36
325	QY	ACTGCTTGATCTCTCAAAAGTGGCGGT-----GCTCCAGCGCGTGGC	284
37	Db	ArgArgSerCysThrSerAlaProArgCysHisArgIleAlaProGlyVargGly	56

283	Qy	-----CCTTGACCAGATGGCGTGTGGTTCGTACATGC	251
57	Db	ArgCysArgGlyArgHisArgArgGlyAlaProAlaArgLysArgArgCys	76
250	Qy	TTGGGCCCTTGTATTGGTCTGCTCGCCAAACACGAAGCTCATGAACCTTGACCTGCTTCA	191
77	Db	SerGly-----SerAlaAlaArgArgArgSer-----Gly	88
190	Qy	TCCTCTGCTCTTGCATGTCCA-----GGGACTCGAAGAAGSGCAGCAGCTCGG	143
89	Db	AlaAlaArgProProCysProArgProGlySerGlyArgArgArgGlyThrAlaPro	108
142	Qy	GGTGAGCCAGCAGCCTTATCTAGTAGAAGGTGTCAACGCCAGCTTCATGCCCTCTGTGGCGCCG	83
109	Db	GlySerProArgGlyArgArgArgArgThrHisPro-----ArgArg	122
82	Qy	CCAGGTCAATCAACAGCTTCTTGTGCCCGC-----ATCCGCGTT	44
123	Db	GluGly-----GlyProCysThrArgArgSerArgArgGlySerProProArg	139
43	Qy	CCGCGCTCTGTGTGTGTGGCGG	17
140	Db	ProProSerCysThrCvsLeuValPro	148

RESULT 14

```

US-10-437-963-141171
; Sequence 141171, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 141171
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42300C.1.pep
US-10-437-963-141171

```

Alignment Scores:		
Pred. No.:	0.0274	Length:
Score:	115.50	Matches:
Percent Similarity:	32.74%	Conservative:
Best Local Similarity:	27.43%	Mismatches:
Query Match:	10.82%	Indels:
DB:	16	Gaps:
		224

US-09-920-953-2 (1-598) x US-10-437-963-141171 (1-224)

Qy	2	CGTGCCTG	CAGACGCGGCCAC	CAGACACAGACGCGGAGCGGATGCGGCGCA	61	
Db	12	ArgAlaLeu	GlnArg-His	GlyHisArgHisGlyArgArgGlyAlaArg	29	
Qy	62	AGAAGCTG	TTTTCATGACCT	GCGCGCGCAGAGGCATGAA	GCTGGCGGTGCACCTTCT	121
Db	30	-----	-----	GlyArgT	ArgArgArgGlyGlyGlyGlnAlaAsnAr	43
Qy	122	ACGATAAG	TGCTGGCTGAC	CCGGAGCTGCTGCCCTT	CTTGAGTGCCTTGGACATGC	181
Db	43	aArgPro	ProArgHisPro	ProSerCvsArgGlnArgArgArgArgPro	aArgArgArgArgAr	63

182	A	-----GCAGAGATGAAGCAGAGTCAAGTTTCATGAGCTTCGTCTGTTGGCG	222
Qy			
Db			
63	gProAlaLeuArgProAlaGlyAlaHisAlaGlyArgValArgProLeuAlaLeuAlaArg	83	
Qy			
Db			
227	GAGCAGACCAATACAAGGGCCGAGCATGTACACGCACACAGCCCA	272	
Qy			
Db			
83	gLeuLeuThrLeuProLeuProArgProProArgValArgGlnProProArgGlyArgAl	103	
Qy			
Db			
273	-----TCTGGTCAAGGGCCACGGCTGGACCGACCGCC	304	
Qy			
Db			
103	aMetLeuLeuArgHisArgArgArgArgGTPArgArgArgArgThrProProPro	123	
Qy			
Db			
305	ACTTTGCACAAGATCAAGCAGTACCTTGGAGA	335	
Qy			
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123	O-----ArgArgArgAlaIleProTPArgValArgArgThrProValHisAlaArgMe	141	
Qy			
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336	-----GACGCTGCA	361	
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141	tAlaAlaGlyAlaAlaValProAlaThrGlyAspArgArgArgArgGlyArgArgAl	161	
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362	AGGATGTGATCCAGCACGCCGCCGAGTGTGTGA	415	
Qy			
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161	aAlaAlaLeuProGluAlaHisArgSerGlyGlyArgAlaValValProArg	178	
Qy			
Db			
416	ACTTNCCCAACACTGGCGCACCCCACTGATTTTCATTAACCCACCCCGCTGAGCGCT	475	
Qy			
Db			
178	-----	178	
Qy			
Db			
476	CATTCCTCATCGATTTTGTAGCGGGGAGCGCCAG	517	
Qy			
Db			
179	-LeuProArgArgValGlnGlyGlyArgHisAlaGlyHisAlaGlyValLeuProPro	198	
Qy			
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518	GCCACGGGGGCCAGG	533	
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198	aArgArgAlaProArg	203	
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RESULT 15

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US-10-425-114-63797
; Sequence 63797, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Sreen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63797
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-OSFLM202018F10_FLI.pep
; US-10-425-114-63797

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Alignment Scores:	
Pred. No.:	0.0341
Score:	115.50
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Conservative:	16
Mismatches:	80
Best Local Similarity:	28.31%
Query Match:	10.82%
Indels:	61
Gaps:	10
DB:	15
Length:	517

US-08-020-953-2 (1-598) x US-10-425-114-63797 (1-517)

QY 24 CAGCACCAACAGAGACGGCGGA-----AGCGGGATG 53
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Fri Feb 25 16:26:58 2005

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Db      89 ArgHisGlyArgAspAlaGlyGlyGluProArgHisProAlaAspArgThrAlaGlyArg 108
QY      54 CGGGCGCAAGACTGTTGATGACCTGGCGCGCGCAGAGGCATGAAGCTGGCGGTGA 113
Db      109 HisAlaAspArgGlyGlnHisValProGlyArgArgAlaArgGluArgArgGlyGln 128
QY      114 CACCTT-----CTACGATAAGTGTGCTGACCCCGAGCTGCTGCCCTTCTTGA 164
Db      129 HisCysHisAlaHisHisArgGluAspAlaAlaTrpProGlyAlaArgValLeu----- 146
QY      165 GTCCCTGGACATGCA-----AGACA 185
Db      147 GlyProGlyHisAlaGlyValProArgArgAspValAlaAlaValAlaArgArgVal 166
QY      186 GAAGATGAAGCAGGTCAGTTCATGCTTCGTTGCGCGAGCAGCAACCAATACAAGG 245
Db      167 HisLeuArgLeuProAlaValHisGlnArgValProHisArgGlnProAspGln--- 185
QY      246 CGAAGCATGTACGAGC-----ACAGCCCATCTGCT--- 278
Db      186 LeuArgHisValAlaAspProArgValGlyMetAlaProValAlaAlaArgProArgGlyVal 205
QY      279 -----CAAGGGCCAGGCTGACCCACCGCCACTTTGACAGATCAAGCAGTA 326
Db      206 ProGlyArgArgHisGlyGlyArgArgGlyValHisProGlyHisAlaGlnProGly 225
QY      327 CCTTGGAGAGCGCT-----GCAAGAGATGGCGT 356
Db      226 ProAlaArgGluAlaArgProArgProArgArgAlaProAlaGlyAlaArgGlnGlyArg 245
QY      357 CAAGCAGGATGTATCCAGCAGCCCGCGAGTGGTGGAGTCCACCCGCGAGCAATTGA 416
Db      246 Arg-----ArgArgArgValGlnArgHisProArgArgArgGly 259
QY      417 CTNCCCAACTGCGCACCACTGATTTTCATTACCCCAACCCCGCTGAGCGTC 476
Db      260 AlaArgProGlnGluArgArgGlyArgValProAlaAspProAla-----AlaArg 276
QY      477 ATTCATCGATTGAGCGGAGCGCCAGTTGCGCGAGCGCGCCAGGGGCCAGG 533
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Search completed: February 22, 2005, 21:26:11
Job time : 129 secs